

GenCore version 5.1.8  
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## OM protein - protein search, using sw mode!

Run on: May 15, 2006, 16:16:32 ; Search time 47 Seconds  
(without alignments)

28.145 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNRWEDPGKQLYNEA 16

Scoring table: BLOSUM62

Gapext 0.5

Searched: 572060 seqs, 8275679 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
 1: /cggn2\_6/ptodata/1/iaa/5\_COMB.pep:/\*  
 2: /cggn2\_6/.ptodata/1/iaa/6\_COMB.pep:/\*  
 3: /cggn2\_6/.ptodata/1/iaa/H\_COMB.pep:/\*  
 4: /cggn2\_6/ptodata/1/iaa/PICTUS\_COMB.pep:/\*  
 5: /cggn2\_6/.ptodata/1/iaa/RE\_COMB.pep:/\*  
 6: /cggn2\_6/.ptodata/1/iaa/backfile1.pep:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	91	100.0	16	2	US-09-070-907-1	Sequence 1, Appli
2	91	100.0	16	2	US-09-623-548A-1536	Sequence 1536, AP
3	91	100.0	16	2	US-09-657-276-1536	Sequence 1536, AP
4	91	100.0	63	1	US-08-447-411-24	Sequence 24, Appli
5	91	100.0	63	1	US-08-447-411-63	Sequence 63, Appli
6	91	100.0	63	1	US-08-662-227-20	Sequence 20, Appli
7	91	100.0	63	2	US-09-925-442-20	Sequence 20, Appli
8	91	100.0	310	2	US-09-834-309-7	Sequence 7, Appli
9	91	100.0	310	2	US-09-834-309-8	Sequence 8, Appli
10	91	100.0	310	2	US-09-834-309-9	Sequence 9, Appli
11	91	100.0	1663	1	US-08-793-126-1	Sequence 1, Appli
12	91	100.0	1663	2	US-09-132-271-1	Sequence 1, Appli
13	91	100.0	1663	2	US-09-142-334-42	Sequence 22, Appli
14	91	100.0	1663	2	US-08-447-411-26	Sequence 26, Appli
15	80	87.9	63	1	US-08-447-411-27	Sequence 27, Appli
16	79	86.8	63	1	US-08-447-411-35	Sequence 28, Appli
17	73	80.2	308	2	US-09-582-761B-26	Sequence 26, Appli
18	73	80.2	330	2	US-09-582-761B-37	Sequence 37, Appli
19	73	80.2	929	2	US-09-582-761B-27	Sequence 21, Appli
20	73	80.2	65.9	11	US-09-039-060A-6	Sequence 6, Appli
21	60	65.9	11	2	US-08-495-606E-37	Sequence 37, Appli
22	60	65.9	11	4	PCT-US94-01234-37	Sequence 31, Appli
23	60	65.9	11	4	PCT-US94-01263-76	Sequence 7, Appli
24	60	65.9	11	4	US-08-447-411-76	Sequence 76, Appli
25	52	57.1	1333	1	US-08-662-227-34	Sequence 34, Appli
26	52	57.1	1333	2	US-09-017-947-34	Sequence 34, Appli

## ALIGNMENTS

RESULT 1  
US-09-070-907-1  
; Sequence 1, Application US/09070907  
; Patent No. 6238667  
; GENERAL INFORMATION:  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: METHOD OF AFFINITY CROSS-LINKING BIOLOGICALLY ACTIVE PEPTIDES TO ANTIBODIES.  
; FILE REFERENCE: 35629  
; CURRENT APPLICATION NUMBER: US/09-070-907  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Patentin Ver. 2.0 - beta  
SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence AMINO ACID  
US-09-070-907-1

Query Match Score 91; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.4e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEA 16  
Db 1 KNRWEDPGKQLYNEA 16

RESULT 2  
US-09-623-548A-1536  
; Sequence 1536, Application US/09623548A  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Bzrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09-623-548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17

PRIOR APPLICATION NUMBER: 60/153,406  
 PRIOR FILING DATE: 1999-09-10  
 PRIOR APPLICATION NUMBER: 60/159,783  
 PRIOR FILING DATE: 1999-10-18  
 NUMBER OF SEQ ID NOS: 1617  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1536  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-09-623-549A-1536

Query Match Score 91; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNEA 16  
 Db 1 KNRWEDPGKOLYNEA 16

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**RESULT 3**  
 US-09-637-276-1536  
 Sequence 1536, Application US/09657276  
 Patent No. 6887470

GENERAL INFORMATION:  
 APPLICANT: Conjuchen, Inc.  
 APPLICANT: Bridon, Dominique  
 APPLICANT: Ezrin, Alan  
 APPLICANT: Milner, Peter  
 APPLICANT: Holmes, Darren  
 APPLICANT: Thibaudeau, Karen

TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
 TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
 TITLE OF INVENTION: COMPONENTS  
 FILE REFERENCE:  
 CURRENT APPLICATION NUMBER: US/09/657,276  
 CURRENT FILING DATE: 2000-09-07  
 PRIOR APPLICATION NUMBER: 60/134,406  
 PRIOR FILING DATE: 1999-05-17  
 PRIOR APPLICATION NUMBER: 60/153,406  
 PRIOR FILING DATE: 1999-09-10  
 PRIOR APPLICATION NUMBER: 60/159,783  
 PRIOR FILING DATE: 1999-10-18  
 NUMBER OF SEQ ID NOS: 1617  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1536  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-09-637-276-1536

Query Match Score 91; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNEA 16  
 Db 9 KNRWEDPGKOLYNEA 24

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**RESULT 4**  
 US-08-447-411-24  
 Sequence 24, Application US/08447411  
 Patent No. 5773243

GENERAL INFORMATION:  
 APPLICANT: FRITZINGER, DAVID C.

APPLICANT: BREDEHORST, REINHARD  
 APPLICANT: VOGEL, CARL-WILHELM  
 TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2  
 NUMBER OF SEQUENCES: 91  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: P.C.  
 STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/447,411  
 FILING DATE:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/043,747  
 FILING DATE: 07-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Obion, No. 5773243man F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE DOCKET NUMBER: 1126-101-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 TELEX: 248555 PAT UR  
 INFORMATION FOR SEQ ID NO: 63:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 63 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 S-08-447-11-63

RESULT 6  
 US-08-662-227-20  
 Sequence 20, Application US/08662227  
 Patent No. 592320  
 GENERAL INFORMATION:  
 APPLICANT: VOGEL, CARL-WILHELM  
 PREDEHORST, REINHORST  
 APPLICANT: ROCK, MICHAEL  
 APPLICANT: FRITZINGER, DAVID  
 TITLE OF INVENTION: RECOMBINANT PROCVF  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBILO, SPIVAR, MCCLELLAND, MAIER & N  
 ADDRESS: P.C.  
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/662,227  
 FILING DATE: 14-JUN-1996  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBION, NORMAN F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE DOCKET NUMBER: 1126-0107-0X  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: 703-413-3000  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 63 amino acids

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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-662-227-20

Query Match          100 0%; Score 91; DB 1; Length 63;
Best Local Similarity 100 0%; Pred. No. 3.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 KNRWEDPGKQLYNEA 16
Db      9 KNRWEDPGKQLYNEA 24

RESULT 7
US-09-017-947-20
; Sequence 20. Application US/09017947
; Patent No. 6303754
GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P. C.
; STREET: 1756 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,947
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/662,227
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-017-947-20

Query Match          100 0%; Score 91; DB 2; Length 63;
Best Local Similarity 100 0%; Pred. No. 3.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 KNRWEDPGKQLYNEA 16
Db      9 KNRWEDPGKQLYNEA 24

RESULT 8
US-09-025-442-20

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Sequence 20, Application US/09925442  
 Patent No. 6607837  
 GENERAL INFORMATION:  
 APPLICANT: VOGEL, CARL-WILHELM BREDEHORST, REINHORST KOCK, MICHAEL FRITZINGER, DAVID  
 TITLE OF INVENTION: RECOMBINANT PROCVCF  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 P.C.  
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/925,442  
 FILING DATE: 10-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION NUMBER: 09/017,947  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 1126-0107-0X  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 63 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
 US-09-925-442-20

Query Match Score 91; DB 2; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEA 16  
 Db 9 KNRWEDPGKQLYNEA 24

RESULT 9  
 US-09-834-309-7  
 Sequence 7, Application US/09834309  
 Patent No. 6820011  
 GENERAL INFORMATION:  
 APPLICANT: Chen, Xiaojiang  
 TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE  
 FILE REFERENCE: 2848-43  
 CURRENT APPLICATION NUMBER: US/09/834,309  
 CURRENT FILING DATE: 2001-04-11  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: Patentn version 3.0  
 SEQ ID NO: 7  
 LENGTH: 310  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-09-834-309-8  
 Sequence 8, Application US/09834309  
 Patent No. 6820011  
 GENERAL INFORMATION:  
 APPLICANT: Chen, Xiaojiang  
 APPLICANT: Holers, V. Michael  
 TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND US  
 FILE REFERENCE: 2848-43  
 CURRENT APPLICATION NUMBER: US/09/834,309  
 CURRENT FILING DATE: 2001-04-11  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: Patentn version 3.0  
 SEQ ID NO: 8  
 LENGTH: 310  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-09-834-309-9  
 Sequence 9, Application US/09834309  
 Patent No. 6820011  
 GENERAL INFORMATION:  
 APPLICANT: Chen, Xiaojiang  
 APPLICANT: Holers, V. Michael  
 TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND US  
 FILE REFERENCE: 2848-43  
 CURRENT APPLICATION NUMBER: US/09/834,309  
 CURRENT FILING DATE: 2001-04-11  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: Patentn version 3.0  
 SEQ ID NO: 9  
 LENGTH: 310  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-09-834-309-16  
 Sequence 16, Application US/08793126  
 Patent No. 5849297

RESULT 12  
 US-08-793-126-1  
 Sequence 1, Application US/08793126  
 Patent No. 5849297

GENERAL INFORMATION:  
 APPLICANT: Harrison, Richard Alexander  
 ATTORNEY/AGENT: Farries, Charles Timothy  
 TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HALE AND DORR LLP  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: United States of America  
 ZIP: 02109

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/793,126  
 FILING DATE: 07-FEB-1997  
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
 NAME: Baker, Hollie L.  
 REGISTRATION NUMBER: 31,321  
 REFERENCE/DOCKET NUMBER: 102286.377  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 526-6000  
 TELEFAX: (617) 526-5000  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1663 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-793-126-1

Query Match 100.0%; Score 91; DB 1; Length 1663;  
 Best Local Similarity 100.0%; Prod. No. 1.e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEA 16  
 Db 1217 KNRWEDPGKQLYNEA 1232

RESULT 13  
 US-09-132-271-1  
 ; Sequence 1, Application US/09132271  
 ; Patent No. 622157  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harrison, Richard Alexander  
 ; ATTORNEY/AGENT: Farries, Charles Timothy  
 ; TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HALE AND DORR LLP  
 ; STREET: 60 State Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: United States of America  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; COMPUTER: IBM PC compatible  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/132,271  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/793,126

GENERAL INFORMATION:  
 APPLICANT: Harrison, Richard Alexander  
 ATTORNEY/AGENT: Farries, Charles Timothy  
 TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HALE AND DORR LLP  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: United States of America  
 ZIP: 02109

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/132,271  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/793,126

FILING DATE: 07-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Baker, Hollie L.  
 REGISTRATION NUMBER: 31,321  
 REFERENCE/DOCKET NUMBER: 102286.377  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 526-6000  
 TELEX/FAX: (617) 526-5000  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1663 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-09-132-271-1

Query Match 100.0%; Score 91; DB 2; Length 1663;  
 Best Local Similarity 100.0%; Prod. No. 1.e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEA 16  
 Db 1217 KNRWEDPGKQLYNEA 1232

RESULT 14  
 US-09-142-334-22  
 ; Sequence 22, Application US/09142334  
 ; Patent No. 6263485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harrison, Richard A.  
 ; ATTORNEY/AGENT: Farries, Timothy C.  
 ; TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase  
 ; FILE REFERENCE: 4-20443/A/IMD/PCT  
 ; CURRENT APPLICATION NUMBER: US/09/142,334  
 ; CURRENT FILING DATE: 1999-04-15  
 ; EARLIER APPLICATION NUMBER: PCT/GB97/00603  
 ; NUMBER OF SEQ ID NOS: 35  
 ; EARLIER FILING DATE: 1997-03-04  
 ; SEQ ID NO 22  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; LENGTH: 1663  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-09-142-334-22

Query Match 100.0%; Score 91; DB 2; Length 1663;  
 Best Local Similarity 100.0%; Prod. No. 1.e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEA 16  
 Db 1217 KNRWEDPGKQLYNEA 1232

RESULT 15  
 US-08-447-411-26  
 ; Sequence 26, Application US/08447411  
 ; Patent No. 5773243  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRITZINGER, DAVID C.  
 ; ATTORNEY/AGENT: BREDHORST, REINHARD  
 ; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2  
 ; NUMBER OF SEQUENCES: 81  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESS: P.C.  
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.

ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/447,411  
FILING DATE:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/043,747  
FILING DATE: 07-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblich, No. 577324, Main F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-101-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 24855 OPAT UR  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-447-411-26

Query Match 87.9%; Score 80; DB 1; Length 63;  
Best Local Similarity 81.2%; Pred. No. 2.7e-06;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy	1 KNRMEDPGKOLYNVEA 16
	:   :   :   :
Db	9 RNRMEEPGQQLYNEA 24

Search completed: May 15, 2006, 16:17:50  
Job time : 48 secs



SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 1  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 NAME/KEY: PEPTIDE  
 LOCATION: (1)..(16)  
 OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-1232  
 US-10-795-081A-1

Query Match 100.0%; Score 91; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEVA 16  
 Db 1 KNRWEDPGKQLYNEVA 16

RESULT 3  
 US-11-066-697-1536  
 Sequence 1536, Application US/11066697  
 Publication No. US2005018159A1  
 GENERAL INFORMATION:  
 APPLICANT: Bridon, Dominique P.  
 APPLICANT: Ezrin, Alan M.  
 APPLICANT: Holmes, Darren L.  
 APPLICANT: Milner, Peter G.  
 APPLICANT: Thibaudreau, Karen  
 TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
 TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
 TITLE OF INVENTION: COMPONENTS  
 FILE REFERENCE: 50086200301  
 CURRENT APPLICATION NUMBER: US/11/066,597  
 CURRENT FILING DATE: 2005-02-25  
 PRIOR APPLICATION NUMBER: 09/157,276  
 PRIOR FILING DATE: 2000-09-07  
 PRIOR APPLICATION NUMBER: 60/153,406  
 PRIOR FILING DATE: 1999-09-10  
 PRIOR APPLICATION NUMBER: 60/159,783  
 PRIOR FILING DATE: 1999-10-15  
 NUMBER OF SEQ ID NOS: 1617  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1536  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: Peptide  
 US-11-066-697-1536

Query Match 100.0%; Score 91; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEVA 16  
 Db 1 KNRWEDPGKQLYNEVA 16

RESULT 4  
 US-09-925-442-20  
 Sequence 20, Application US/09925442  
 Patent No. US20050103146A1  
 GENERAL INFORMATION:  
 APPLICANT: VOGEL, CARL-WILHELM  
 BREDEHORST, REINHOLD  
 KOCK, MICHAEL  
 FRITZINGER, DAVID  
 TITLE OF INVENTION: RECOMBINANT PROCVF  
 NUMBER OF SEQUENCES : 39

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 P.C.  
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/925,442  
 FILING DATE: 10-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY INFORMATION DATA:  
 APPLICATION NUMBER: 09/017,947  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 1126-0107-0X

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 63 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
 US-09-925-442-20

Query Match 100.0%; Score 91; DB 3; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEVA 16  
 Db 9 KNRWEDPGKQLYNEVA 24

RESULT 5  
 US-10-424-599-219407  
 Sequence 219407, Application US/10424599  
 Publication No. US2004031072A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa Thomas J  
 APPLICANT: Kovacic David K  
 APPLICANT: Zhou Yihua  
 APPLICANT: Cao Yongwei  
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 FILE REFERENCE: 38-21(53223)B  
 CURRENT APPLICATION NUMBER: US/10/424,599  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 285684  
 SEQ ID NO 219407  
 LENGTH: 94

TYPE: PRT  
 ORGANISM: Glycine max  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (1)..(94)  
 OTHER INFORMATION: unsure at all xaa locations  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT3847\_40150C.1.pep  
 US-10-424-599-219407

Query Match 100.0%; Score 91; DB 4; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEA 16  
 Db 43 KNRWEDPGKQLYNEA 58

RESULT 6

US-09-834-309-7  
 Sequence 7, Application US/09834309  
 Publication No. US20040005538A1

GENERAL INFORMATION:  
 APPLICANT: Holers, V. Michael  
 TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE  
 TITLE OF INVENTION: THEREOF  
 FILE REFERENCE: 2848-43  
 CURRENT APPLICATION NUMBER: US/09/834,309  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 9  
 LENGTH: 310  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-834-309-9

Query Match 100.0%; Score 91; DB 3; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEA 16  
 Db 224 KNRWEDPGKQLYNEA 239

RESULT 9

US-10-379-747-4  
 Sequence 4, Application US/10379747  
 Publication No. US2004002387A1

GENERAL INFORMATION:  
 APPLICANT: Burgess, Catherine E.;  
 APPLICANT: Chant, John S.;  
 APPLICANT: Chaudhuri, Amitabha;  
 APPLICANT: Edinger, Shlomit R.;  
 APPLICANT: Gangolli, Esha A.;  
 APPLICANT: Malyankar, Uriel M.;  
 APPLICANT: Miller, Charles E.;  
 APPLICANT: Ooi, Chean Eng;  
 APPLICANT: Ort, Tatiana A.;  
 APPLICANT: Paturlajan, Meera;  
 APPLICANT: Rastelli, Luca;  
 APPLICANT: Rieger, Daniel K.;  
 APPLICANT: Shimkets, Richard A.;  
 APPLICANT: Zerhusen, Bryan D.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 FILE REFERENCE: 21402-56B  
 CURRENT APPLICATION NUMBER: US/10/379,747  
 CURRENT FILING DATE: 2003-03-05  
 PRIOR APPLICATION NUMBER: 60/365,034  
 PRIOR FILING DATE: 2002-03-15  
 PRIOR APPLICATION NUMBER: 60/366,420  
 PRIOR FILING DATE: 2002-03-21  
 PRIOR APPLICATION NUMBER: 60/365,477  
 NUMBER OF SEQ ID NOS: 45  
 SOFTWARE: Curaseqist version 0.1  
 SEQ ID NO 4  
 LENGTH: 705  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-379-747-4

Query Match 100.0%; Score 91; DB 4; Length 705;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNEA 16  
 Db 259 KNRWEDPGKQLYNEA 274

RESULT 8

US-09-834-309-9  
 Sequence 9, Application US/09834309  
 Publication No. US20040005538A1

GENERAL INFORMATION:  
 APPLICANT: Chen, Xiaojiang

GENERAL INFORMATION:  
; APPLICANT: MESSER, Jeffrey  
; APPLICANT: BENJAMIN, Dennis  
; APPLICANT: VATH, James  
; APPLICANT: SIGEL, Eric  
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; TITLE OF INVENTION: ENDOMETRIOSIS  
; FILE REFERENCE: PPI-149  
; CURRENT APPLICATION NUMBER: US/10/887,775  
; CURRENT FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: 60/486,379  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: 60/533,430  
; PRIOR FILING DATE: 2003-12-29  
; PRIOR APPLICATION NUMBER: 60/575,269  
; PRIOR FILING DATE: 2004-05-08  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 935  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-887-775-32

Query Match 100.0%; Score 91; DB 5; Length 935;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05; Indels 0; Gaps 0;

Qy 1 KNRMEDPGKOLYNEA 16  
Db 489 KNRMEDPGKOLYNEA 504

RESULT 11  
US-10-497-073-17  
; Sequence 1, Application US/10497073  
; Publication No. US20050044584A1  
; GENERAL INFORMATION:  
; APPLICANT: Biovision AG  
; TITLE OF INVENTION: Method for detecting Alzheimer's disease and differentiating  
; TITLE OF INVENTION: Alzheimer's disease from other demental diseases, associated  
; TITLE OF INVENTION: peptides and the use thereof  
; FILE REFERENCE: C3 F-PCT  
; CURRENT APPLICATION NUMBER: US/10/497,073  
; CURRENT FILING DATE: 2004-05-18  
; PRIOR APPLICATION NUMBER: DE10158180  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: PCT/DE02/04350  
; PRIOR FILING DATE: 2002-11-27  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 1255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-497-073-17

Query Match 100.0%; Score 91; DB 5; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05; Indels 0; Gaps 0;

Qy 1 KNRMEDPGKOLYNEA 16  
Db 809 KNRMEDPGKOLYNEA 824

RESULT 12  
US-10-741-600-1326  
; Sequence 126, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1326  
; LENGTH: 1288  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-741-600-1326

Query Match 100.0%; Score 91; DB 5; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05; Indels 0; Gaps 0;

Qy 1 KNRMEDPGKOLYNEA 16  
Db 1217 KNRMEDPGKOLYNEA 1232

RESULT 13  
US-10-450-763-56335  
; Sequence 56335, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790C1TP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
SEQ ID NO 56335  
; LENGTH: 1540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (689)..(699)  
; OTHER INFORMATION: ANAPHYLATOXIN DOMAIN SIGNATURE domain identified by eMATRIX,  
; OTHER INFORMATION: accession number PR00004A, p-value=5.500e-13, raw score of 9.52  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (756)..(1370)  
; OTHER INFORMATION: Alpha-2-macroglobulin family domain identified by PFam,  
; OTHER INFORMATION: accession name A2M, E-value=0, Pfam score of 1156.5  
US-10-450-763-56335

Query Match 100.0%; Score 91; DB 5; Length 1540;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05; Indels 0; Gaps 0;

Qy 1 KNRMEDPGKOLYNEA 16  
Db 1217 KNRMEDPGKOLYNEA 1232

RESULT 14  
US-10-884-813-8  
; Sequence 8, Application US/10884813  
; Publication No. US2005079585A1  
; GENERAL INFORMATION:  
; APPLICANT: Kolin, Johanna  
; Bredenhorst, Reinhard  
; APPLICANT: Spillner, Edzard

; TITLE OF INVENTION: Complement Depletion with Recombinant Human C3 Derivatives  
 ; FILE REFERENCE: P 63782  
 ; CURRENT APPLICATION NUMBER: US/10/884,813  
 ; CURRENT FILING DATE: 2004-07-02  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 8  
 ; LENGTH: 1638  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybrid protein  
 US-10-884-813-8

Query Match 100.0%; Score 91; DB 5; Length 1638;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KNRWEDPGKQLYNVEA 16  
 Db 1217 KNRWEDPGKQLYNVEA 1232

RESULT 15  
 US-10-884-813-12  
 ; Sequence 12, Application US/10884813  
 ; Publication No. US20050079585A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kolln, Johanna  
 ; APPLICANT: Bredehorst, Reinhard  
 ; APPLICANT: Spillner, Edzard  
 ; TITLE OF INVENTION: Complement Depletion with Recombinant Human C3 Derivatives  
 ; FILE REFERENCE: P 63782  
 ; CURRENT APPLICATION NUMBER: US/10/884,813  
 ; CURRENT FILING DATE: 2004-07-02  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 12  
 ; LENGTH: 1638  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybrid protein  
 US-10-884-813-12

Query Match 100.0%; Score 91; DB 5; Length 1638;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KNRWEDPGKQLYNVEA 16  
 Db 1217 KNRWEDPGKQLYNVEA 1232

Search completed: May 15, 2006, 16:31:27  
 Job time : 165 secs

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; PRIORITY FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-415-8

Query Match          100.0%;  Score 91;  DB 9;  Length 310;
Best Local Similarity 100.0%;  Pred. No. 1.2e-07;  Indels 0;  Gaps 0;
Matches 16;  Conservative 0;  Mismatches 0;  Other INFORMATION: complement component C3 precursor
Qy      1 KNRWEDPGKQLYNEA 16
Db     224 KNRWEDPGKQLYNEA 239

RESULT 3
US-10-921-415-9
Sequence 9, Application US/10921415
Publication No. US20060014681A1
GENERAL INFORMATION:
APPLICANT: Chen, Xiaojiang
TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
FILE REFERENCE: 2848-43
CURRENT APPLICATION NUMBER: US/10/921,415
PRIORITY FILING DATE: 2004-08-16
PRIORITY APPLICATION NUMBER: US/09/834,309
PRIORITY FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 9
LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapiens
US-10-921-415-9

Query Match          100.0%;  Score 91;  DB 9;  Length 310;
Best Local Similarity 100.0%;  Pred. No. 1.2e-07;  Indels 0;  Gaps 0;
Matches 16;  Conservative 0;  Mismatches 0;  Other INFORMATION: desarg peptide
Qy      1 KNRWEDPGKQLYNEA 16
Db     224 KNRWEDPGKQLYNEA 239

RESULT 4
US-10-982-545-6
Sequence 6, Application US/10982545
Publication No. US2005024490A1
GENERAL INFORMATION:
APPLICANT: Davies, Huw Alun
APPLICANT: McGuire, James
APPLICANT: Simonsen, Anja Hviid
APPLICANT: Blennow, Kaj
APPLICANT: Podust, Vladimir
APPLICANT: Ciphergen Biosystems, Inc.
TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
FILE REFERENCE: 016866-011550US
CURRENT APPLICATION NUMBER: US/10/982,545
CURRENT FILING DATE: 2004-11-06
PRIORITY FILING DATE: 2003-11-07
PRIORITY APPLICATION NUMBER: US 60/518,360
PRIORITY FILING DATE: 2003-12-02
PRIORITY APPLICATION NUMBER: US 60/546,423
PRIORITY FILING DATE: 2004-02-19
PRIORITY APPLICATION NUMBER: US 60/547,250
PRIORITY FILING DATE: 2004-02-23
PRIORITY APPLICATION NUMBER: US 60/558,896

Query Match          100.0%;  Score 91;  DB 11;  Length 1663;
Best Local Similarity 100.0%;  Pred. No. 6.4e-07;  Mismatches 0;  Other INFORMATION: signal peptide
Matches 16;  Conservative 0;  Gaps 0;
Qy      1 KNRWEDPGKQLYNEA 16
Db     224 KNRWEDPGKQLYNEA 239

RESULT 5
US-11-177-506-34
Sequence 34, Application US/11177506
Publication No. US2006029956A1
GENERAL INFORMATION:
APPLICANT: Beyer, Wayne F.
APPLICANT: Venetta, Thomas M.
APPLICANT: Greelke, John W.
APPLICANT: Blaesius, Rainer H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
DETECTION OF OVARIAN DISEASE
FILE REFERENCE: 46143/204851
CURRENT APPLICATION NUMBER: US/11/177,506
CURRENT FILING DATE: 2005-07-08
PRIORITY APPLICATION NUMBER: 60/586,856
PRIORITY FILING DATE: 2004-07-09
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO: 34
LENGTH: 1663
TYPE: PRT
ORGANISM: Homo sapiens
US-11-177-506-34

Query Match          100.0%;  Score 91;  DB 11;  Length 1663;
Best Local Similarity 100.0%;  Pred. No. 6.4e-07;  Mismatches 0;  Other INFORMATION: complement component C3 alpha-chain
Matches 16;  Conservative 0;  Gaps 0;
Qy      1 KNRWEDPGKQLYNEA 16
Db     224 KNRWEDPGKQLYNEA 239

```

Qy 1 KNRMEDPGKQLYNVEA 16  
 Db 1217 KNRMEDPGKQLYNVEA 1232

**RESULT 6**  
 US-10-514-462-11 Application 11, Virus-Like Particles, Methods of Preparation, And Immunogenic  
 Publication No. US20060088909A1

GENERAL INFORMATION:  
 APPLICANT: Emory University  
 TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic  
 CURRENT APPLICATION NUMBER: US/10/514,462  
 CURRENT FILING DATE: 2004-11-12  
 PRIOR APPLICATION NUMBER: 60/5381,557  
 PRIOR FILING DATE: 2002-05-17  
 NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: Patentin version 3.2  
 SEQ ID NO: 11  
 LENGTH: 300  
 TYPE: PRT  
 ORGANISM: C3d sequence  
 US-10-514-462-11

Query Match 80.2%; Score 73; DB 8; Length 300;  
 Best Local Similarity 75.0%; Pred. No. 0.00012; Indels 0; Gaps 0;  
 Matches 12; Conservative 3; Mismatches 1;

Qy 1 KNRMEDPGKQLYNVEA 16  
 Db 197 RNWEEEPQDQQLYNVEA 212

**RESULT 7**  
 US-11-079-463-5775 Application 5775, Nucleic Acid and Amino Acid Sequences Relating to Bacteroides Fra  
 Publication No. US20060073161A1

GENERAL INFORMATION:  
 APPLICANT: Gary L. Breton  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA  
 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: PATH0-03DIV2  
 CURRENT APPLICATION NUMBER: US/11/079,463  
 CURRENT FILING DATE: 2005-03-14  
 PRIOR APPLICATION NUMBER: US 60/128,705  
 PRIOR FILING DATE: 1999-04-09  
 PRIOR APPLICATION NUMBER: US 09/540,209  
 PRIOR FILING DATE: 2000-04-04  
 NUMBER OF SEQ ID NOS: 10444  
 SEQ ID NO: 5775  
 LENGTH: 347  
 TYPE: PRT  
 ORGANISM: B.fragilis  
 US-11-079-463-5775

Query Match 47.3%; Score 43; DB 11; Length 347;  
 Best Local Similarity 63.6%; Pred. No. 14; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 2;

Qy 4 WEDPGKQLYNV 14  
 Db 295 WEDPKQQLSDI 305

**RESULT 8**  
 US-10-514-055-5 Sequence 5, Application US/10514055  
 GENERAL INFORMATION:  
 APPLICANT: CHIRON CORPORATION  
 TITLE OF INVENTION: HIV ENVELOPE-CD4 COMPLEXES AND HYBRIDS

Query Match 47.3%; Score 43; DB 11; Length 591;  
 Best Local Similarity 46.7%; Pred. No. 25;  
 Matches 7; Conservative 4; Mismatches 4;  
 SEQ ID NO: 713 LENGTH: 591  
 TYPE: PRT  
 ORGANISM: Streptococcus pneumoniae TIGR4  
 US-11-188-298-713

Query Match 47.3%; Score 43; DB 11; Length 591;  
 Best Local Similarity 46.7%; Pred. No. 25;  
 Matches 7; Conservative 4; Mismatches 4;  
 SEQ ID NO: 15 LENGTH: 591  
 TYPE: PRT  
 ORGANISM: XMRV  
 US-11-188-298-713

Query Match 1 KNRWEEEPQDQQLYNVE 15  
 Db 475 RNKYEDINKHLFGVD 489

RESULT 10  
US-11-188-298-0505  
Sequence 8505, Application US/11188298  
Publication No. US20060075522A1  
GENERAL INFORMATION:  
APPLICANT: Abad, Mark S. et al.  
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-21(53452)B  
CURRENT APPLICATION NUMBER: US/11/188,298  
PRIOR APPLICATION NUMBER: 60/592,978  
PRIOR FILING DATE: 2005-07-22  
NUMBER OF SEQ ID NOS: 22569  
SEQ ID NO: 8505  
LENGTH: 591  
TYPE: PRT  
ORGANISM: *Streptococcus pneumoniae* R6

US-11-188-298-8505

Query Match 47.3%; Score 43; DB 11; Length 591;  
Best Local Similarity 46.7%; Pred. No. 25;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVE 15  
Db 475 KNKYEDTNKHLFGVD 489

RESULT 11  
US-11-188-298-10639  
Sequence 10639, Application US/11188298  
Publication No. US20060075522A1  
GENERAL INFORMATION:  
APPLICANT: Abad, Mark S. et al.  
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-21(53452)B  
CURRENT APPLICATION NUMBER: US/11/188,298  
PRIOR APPLICATION NUMBER: 60/592,978  
PRIOR FILING DATE: 2005-07-22  
NUMBER OF SEQ ID NOS: 22569  
SEQ ID NO: 10639  
LENGTH: 591  
TYPE: PRT  
ORGANISM: *Streptococcus pneumoniae*

US-11-188-298-10639

Query Match 47.3%; Score 43; DB 11; Length 591;  
Best Local Similarity 46.7%; Pred. No. 25;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVE 15  
Db 475 KNKYEDTNKHLFGVD 489

RESULT 12  
US-11-188-298-13585  
Sequence 13585, Application US/11188298  
Publication No. US20060075522A1  
GENERAL INFORMATION:  
APPLICANT: Abad, Mark S. et al.  
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-21(53452)B  
CURRENT APPLICATION NUMBER: US/11/188,298  
CURRENT FILING DATE: 2005-07-22  
PRIOR APPLICATION NUMBER: 60/592,978  
NUMBER OF SEQ ID NOS: 22569  
SEQ ID NO: 13585  
LENGTH: 591  
TYPE: PRT

Query Match 47.3%; Score 43; DB 11; Length 842;  
Best Local Similarity 54.5%; Pred. No. 35;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NRWEDPGKOLY 12  
Db 410 NRWQEVGKAMY 420

---

; ORGANISM: *Streptococcus pneumoniae*  
US-11-188-298-13585  
Query Match 47.3%; Score 43; DB 11; Length 591;  
Best Local Similarity 46.7%; Pred. No. 25;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVE 15  
Db 475 KNKYEDTNKHLFGVD 489

RESULT 13  
US-11-188-298-1487  
Sequence 1487, Application US/11188298  
Publication No. US20060075522A1  
GENERAL INFORMATION:  
APPLICANT: Abad, Mark S. et al.  
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-21(53452)B  
CURRENT APPLICATION NUMBER: US/11/188,298  
CURRENT FILING DATE: 2005-07-22  
PRIOR APPLICATION NUMBER: 60/592,978  
PRIOR FILING DATE: 2004-07-31  
NUMBER OF SEQ ID NOS: 22569  
SEQ ID NO: 1487  
LENGTH: 655  
TYPE: PRT  
ORGANISM: *Clostridium tetani* E88

US-11-188-298-1487

Query Match 47.3%; Score 43; DB 11; Length 655;  
Best Local Similarity 46.7%; Pred. No. 27;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVE 15  
Db 385 KNWKEELNRLFNTIE 399

RESULT 14  
US-11-100-356-2  
Sequence 2, Application US/11100356  
Publication No. US2006007115A1  
GENERAL INFORMATION:  
APPLICANT: ZUR MEGDE, Jan  
APPLICANT: BARRETT, Susan  
APPLICANT: LIAN, Ying  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B  
FILE REFERENCE: 2300-162120  
CURRENT APPLICATION NUMBER: US/11/100,356  
CURRENT FILING DATE: 2005-04-06  
PRIOR APPLICATION NUMBER: US/10/190,434  
PRIOR FILING DATE: 2002-07-05  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: PatentIn Ver. 2.0  
SBQ ID NO: 2  
LENGTH: 842  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: SF162

US-11-100-356-2

Query Match 47.3%; Score 43; DB 11; Length 842;  
Best Local Similarity 54.5%; Pred. No. 35;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NRWEDPGKOLY 12  
Db 410 NRWQEVGKAMY 420

RESULT 15  
US-10-514-462-1  
Sequence 1, Application US/1014462  
Publication No. US20060088909A1  
GENERAL INFORMATION  
APPLICANT: Emory University  
TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic  
TITLE OF INVENTION: Compositions  
FILE REFERENCE: 050508-2210  
CURRENT APPLICATION NUMBER: US/10/514,462  
CURRENT FILING DATE: 2004-11-12  
PRIOR APPLICATION NUMBER: 60/381,557  
PRIOR FILING DATE: 2002-05-17  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO: 1  
LENGTH: 847  
TYPE: PRT  
ORGANISM: HIV SF162 Envelope Protein  
US-10-514-462-1

Query Match 47.3%; Score 43; DB 8; Length 847;  
Best Local Similarity 54.5%; Prod. No. 36;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
On 2 NRWEDPGKOLY 12  
Db 415 NRWQEVGKAMY 425

Search completed: May 15, 2006, 16:35:07  
Job time : 29 secs

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OM protein - protein search, using sw model

Run on: May 15, 2005, 16:12:36 ; Search time 38 Seconds  
 (without alignments)  
 40.512 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNRNEDPGKOLYNVEA 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing First 45 summaries

Database : PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match	Length	DB	ID	Description
1	91	100.0	1663	1	C3HU		complement C3 precursor [validated] - human
2	80	87.9	1663	1	C3RT		N-Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit; C;Species: Homo sapiens (man)
3	79	86.8	726	2	A27802		C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 09-Jul-2004
4	73	80.2	1663	1	C3MS		C;Accession: A90065; A37999; R32187; A27803; A23435; A45830; B45830; A01257; A01258
5	58	63.7	1666	1	C3GP		Ride Bruijn, M.H.L.; Fey, G.H.
6	52	57.1	1358	2	B86241		Proc. Natl. Acad. Sci. U.S.A. 82, 708-712, 1985
7	44.5	48.9	490	2	D71401		A;Title: Human complement component C3: cDNA coding sequence and derived primary structure of gene
8	44	48.4	590	2	A44068		A;Reference number: A94065; MUID: 85140166; PMID: 2579379
9	43	47.3	590	2	G82153		A;Molecule type: mRNA
10	43	47.3	432	2	T05236		A;Residues: 1-1663 <DEB>
11	43	47.3	591	2	B97952		A;Cross-references: UNIPARC:UPI000047168; GB:K02765; NID:9179664; PIDN:R32187; A27803; A23435; A45830; B45830; A01257; A01258
12	43	47.3	591	2	F95084		R;Vik, D.P.; Amiguet, P.; Moffat, G.J.; Fey, M.; Amiguet-Barras, F.; Wetsel, R.A.; Tack, Biochemistry 30, 1080-1085, 1991
13	43	47.3	852	2	T12016		A;Title: Structural features of the human C3 gene: intron/exon organization, transcript A;Reference number: A37999; MUID: 91113687; PMID: 1703437
14	43	47.3	1651	1	C3NJ		A;Contents: intron/exon structure of gene
15	42.5	46.7	537	2	B90598		A;Accession: A37999
16	42	46.2	923	2	E83574		A;Residues: 1-25 <VIK>
17	41	45.1	359	2	S45700		A;Cross-references: UNIPARC:UPI0000150417
18	41	45.1	538	2	E85438		R;Daoudak, M.E.; Becherer, J.D.
19	41	45.1	574	2	T16230		J. Immunol. 140, 1577-1580, 1988
20	41	45.1	2166	2	G70163		A;Title: A 34-amino acid peptide of the third component of complement mediates properdin; A;Reference number: A27603; MUID: 88154452; PMID: 3279119
21	41	45.1	5138	2	B96695		A;Accession: A27603
22	40.5	44.5	400	1	JC1428		A;Molecule type: protein
23	40	44.0	166	2	A85077		A;Residues: 1409-1563 <DAO>
24	40	44.0	274	2	S75320		A;Cross-references: UNIPARC:UPI0000173215
25	40	44.0	290	2	G82360		R;Hellman, U.; Eggertsen, G.; Engstrom, A.; Sjoquist, J.
26	40	44.0	311	2	C89894		A;Title: Amino acid sequence of the trypsin-generated C3d fragment from human complement
27	40	44.0	331	2	A12972		A;Reference number: A23435; MUID: 86025442; PMID: 3876831
28	40	44.0	331	2	B98310		A;Molecule type: protein
29	40	44.0	359	1	RGHUGY		A;Residues: 1002-1012,'E',1014-1303 <HEL>

A;Cross-references: UNIPARC:UPI0000173216

A;Note: sequence corresponds to residues 1072-1100 was not determined but was taken E, R;Poznansky, M.C.; Cissold, P.M.; Lachmann, P.J.

J. Immunol. 143, 1254-1258, 1989

A;Title: The difference between human C3F and C3S results from a single amino acid change  
3.  
A;Reference number: A45830; MUID:89309808; PMID:2473125  
A;Accession: A45830  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1212-1215 'N' 1217-1223 <POZ>  
A;Cross-references: UNIPARC:UPI0000173217  
A;Note: this is the C3S allele  
A;Accession: B45830  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1212-1223 <POZ>  
A;Cross-references: UNIPARC:UPI0000173218  
R;Dolmer, K.; Sottrup-Jensen, L.  
FEBS Lett. 315, 85-90, 1993  
A;Title: Disulfide bridges in human complement component C3b.  
A;Reference number: S27041; MUID:93105233; PMID:8416818  
A;Contents: annotation  
C;Comment: The sequence shown is the C3 fast (C3F) allele, which is found mainly in Caucasians. Complement C3 contains two chains, formed by removal of four residues and link alternative complement pathways, releases the C3a anaphylatoxin from the amino end of the alternative complement pathway C3/C5 convertase.  
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.  
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign particles. Classical complement pathway C3/C5 convertase. The activity of C3b is regulated by protease inhibitors. The major site of synthesis of this plasma protein is the liver.  
C;Genetics:  
A;Gene: GDB:C3  
A;Cross-references: GDB:119044; OMIM:120700  
A;Map position: 19p13.3-19p13.3  
A;Note: contains 41 exons  
C;Superfamily: alpha-2-macroglobulin  
C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein; P1-22/Domain: signal sequence #status predicted <SG>  
P;23-667-67-1663/Product: complement C3 and C5b beta chain #status predicted <C3BB>  
P;23-667-74-1663/Product: complement C3 #status predicted <C3C3>  
P;672-1653/Product: complement C3 alpha chain #status predicted <CC3A>  
P;672-748-748/Product: C3a anaphylatoxin #status predicted <C3T>  
P;749-1653/Product: C3b alpha' chain #status predicted <C3BA>  
P;946-1303/Product: C3d fragment #status predicted <CDK>  
P;955-1001/Product: C3g fragment #status predicted <CDG>  
P;1002-1303/Product: C3d fragment #status experimental <C3D>  
P;124-1457/Region: prodomain binding  
P;85-939/Binding site: carbohydrate (Asn) (covalent) #status experimental  
P;559-816-227-662-693/Binding site: carboxylic acid (C3 convertase) #status predicted  
P;748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted  
P;1010-1013/Cross-link: thioester (Cys-Gln) #status experimental  
P;1103-1104/Cleavage site: Arg-Ser (complement factor I) #status predicted  
P;1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted  
P;1617/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score: 91; DB: 1; Length: 1663;  
Matches 16; Best Local Similarity 100.0%; Pred. No: 2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNEA 16  
Db 1217 KNRWEDPGKOLYNEA 1232

## RESULT 2

Complement C3 precursor - rat  
N;Alternate names: 37K phospholipase A2 inhibitory protein  
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;  
C;Species: Rattus norvegicus (Norway rat)  
C;Accession: S15764; A54562; A01260; B35979; A35979; EN0567; PN0566; A32281; S08692  
R;Miumi, Y.; Sohda, M.; Ikenara, Y.

Nucleic Acids Res. 18, 2178, 1990  
A;Title: Nucleotide and deduced amino acid sequence of rat complement C3.  
A;Reference number: S15764; MUID:90245672; PMID:2336397  
A;Accession: S15764  
A;Molecule type: mRNA  
A;Residues: 1-1663 <NTIS>  
A;Cross-references: UNIPROT: P01026; UNIPARC:UPI0000127C4B; EMBL:X52477; NID:956953; PID:R.Sundstrom, S.A.; Komm, B.S.; Ponce-de-Leon, H.; Yi, Z.; Teuscher, C.; Lytle, C.R.  
J. Biol. Chem. 264, 16941-16947, 1989  
A;Title: Estrogen regulation of tissue-specific expression of complement C3.  
A;Reference number: A54562; MUID:89380332; PMID:2674144  
A;Accession: A54562  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: P<sup>1</sup>-1316-1595 <SNPN>  
A;Cross-references: UNIPARC:UPI00001708A4; GB:M29866; NID:9203200; PID:AAA00837.1; PID:R.J.Jacobs, J.W.; Rubin, J.S.; Hugli, T.E.; Bogardt, R.A.; Mariz, I.K.; Daniels, J.S.; Dan Biochemistry 17, 5031-5038, 1978  
A;Title: Purification, characterization, and amino acid sequence of rat anaphylatoxin (<A>).  
A;Reference number: A01260; MUID:79062262; PMID:309768  
A;Accession: A01260  
A;Molecule type: protein  
A;Residues: 671-703 'K' 705-720 'KL' 723-748 <JAC>  
A;Cross-references: UNIPARC:UPI0000150418  
A;Note: three disulfide bonds are present  
R;Suwa, Y.; Kudo, T.; Imaizumi, A.; Okada, M.; Kamimura, T.; Suzuki, Y.; Chang, H.W.; Hi Proc. Natl. Acad. Sci. U.S.A. 87, 2395-2399, 1990  
A;Title: Proteinaceous inhibitors of phospholipase A-2 purified from inflammatory sites  
A;Reference number: A35979; MUID:90207203; PMID:2320562  
A;Accession: B35979  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: X<sup>1</sup>-998-1005 <SNW>  
A;Cross-references: UNIPARC:UPI0000173221  
A;Accession: A35979  
A;Molecule type: protein  
A;Residues: X<sup>1</sup>-961-962,'P',964-969 <SU2>  
A;Cross-references: UNIPARC:UPI0000173221  
R;Nakagawa, H.; Komorita, N. Biochem. Biophys. Res. Commun. 194, 1181-1187, 1993  
A;Title: Complement component C3-derived neutrophil chemotactic factors purified from e. A;Reference number: PN0566; MUID:93356786; PMID:8352775  
A;Accession: PN0567  
A;Molecule type: protein  
A;Residues: 568-592 <NAK>  
A;Cross-references: UNIPARC:UPI000008621C  
A;Note: amino end of a C3-derived peptide designated exudate neutrophil chemotactic fac A;Accession: PN0566  
A;Molecule type: protein  
A;Residues: 671-687 <NA2>  
A;Cross-references: UNIPARC:UPI0000088594  
A;Note: amino end of peptide designated neutrophil chemotactic factor 1 and probably id R;Kuivinen, P.C.; Capulong, R.N.; Desombre, E.R. Biochem. Biophys. Res. Commun. 158, 898-905, 1989  
A;Title: The estrogen responsive 110K and 74K rat uterine secretory proteins are struct A;Reference number: A32281; MUID:89149812; PMID:2645873  
A;Accession: A32281  
A;Molecule type: Protein  
A;Residues: 25-41 <KUI>  
A;Cross-references: UNIPARC:UPI0000173223  
A;Experimental source: 17beta-estradiol-stimulated uterus of immature rat  
A;Note: the authors treat this 74K uterine secretory protein, identical as far as sequent C;Comment: Complement C3 contains two chains, formed by removal of four residues and 11 alternative complement pathways, releases the C3a anaphylatoxin from the amino end of rnaactive-complement-pathway C3/C5 convertase.  
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.  
C;Comment: C3b, with its highly reactive chio Group, binds to the surface of foreign protein e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by protein C;Comment: The major site of synthesis of this plasma protein is the liver.  
C;Keywords: acute phase; chemotaxis; complement alternate pathway; complement pathway; F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-666/Product: complement C3 and C3b beta chain #status predicted <C3BB>	
F;25-666/Product: complement C3 #status predicted <CC3>	
F;25-666-749-1663/Product: complement C3 alpha chain #status predicted <C3B>	
F;671-1663/Product: complement C3 alpha chain #status predicted <CC3A>	
F;749-1663/Product: C3a anaphylatoxin #status experimental <C3T>	
F;946-11303/Product: complement C3b alpha <sub>n</sub> chain #status predicted <C3BA>	
F;1002-11303/Product: C3d fragment #status predicted <CD3>	
F;1424-1457/Region: properdin binding	
F;748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted (covalent) #status predicted	
F;939-1617/Binding site: carbohydrate (Asp) #status predicted	
F;1010-1013/Cross-link: thioester (Cys-Gln) #status predicted	
F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted	
F;1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted	
Query Match Score 87.9%; Score 80; DB 1; Length 1663;	
Best Local Similarity 81.2%; Pred. No. 0.00012; Mismatches 0; Indels 0; Gaps 0;	
Matches 13; Conservative 3; Gaps 0;	
Qy 1 KNRWEDPGKQLYNEA 16       :   :            Db 1217 RNRWEEDPGQQLYNEA 1232	
RESULT 3	
A27602 Complement C3 - rabbit (fragment)	
N/Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit	
C:Species: Oryctolagus cuniculus (domestic rabbit)	
C:Date: 15-Dec-1998 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004	
C:Accession: A27602	
R:Kusano, M.; Choi, N.H.; Tomita, M.; Yamamoto, K.; Migita, S.; Sekiya, T.; Nishimura, Immunol. Invest. 15, 365-378, 1986	
A:Title: Nucleotide sequence of cDNA and derived amino acid sequence of rabbit complement C3; Reference number: A27602; PMID:87066907; PMID:3019881	
A:Accession: A27602	
A: Molecule type: mRNA	
A:Residues: 1-726	
A:Cross-references: UNIPROT:P12247; UNIPARC:UP0000127C4D; GB:M32434; NID:g164862; PID:g164862; PID:g164862	
C:Comment: Complement C3 contains two chains, formed by removal of four residues and 11 alternative complement pathways. releases the C3a anaphylatoxin from the amino end of alternative-complement-pathway C3/C5 convertase.	
C:Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.	
C:Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign particles. C:Comment: The major site of synthesis of this plasma protein is the liver.	
C:Comment: The major site of synthesis of this plasma protein is the liver.	
C:Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein	
Query Match Score 86.8%; Score 79; DB 2; Length 726;	
Best Local Similarity 81.2%; Pred. No. 7.5e-05; Mismatches 0; Indels 0; Gaps 0;	
Matches 13; Conservative 3; Gaps 0;	
Qy 1 KNRWEDPGKQLYNEA 16       :   :            Db 280 RNRWEEDPGQQLYNEA 295	
RESULT 4	
C3MS Complement C3 precursor - mouse	
N/Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit	
C:Species: Mus musculus (house mouse)	
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004	
C:Accession: A92459; B92459; A92460; A93918; A21898; A5461; S16369; S16189; I49563; I49563; G.H.	
J. Biol. Chem. 259, 13851-13856, 1984	
A:Title: Structure of murine complement component C3: I. Nucleotide sequence of cloned A:Reference number: A92459; MUID:85054818; PMID:6548745	
A:Accession: A92459	
A:Molecule type: mRNA	
A:Residues: 1-724 <LUJ>	

C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.  
 C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pathogen-associated molecular patterns (PAMPs) and initiates the classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by proteases such as complement factor I and factor H. The major site of synthesis of this plasma protein is the liver.

C;Genetic: c8b:  
 A;Introns: 27/2; 90/3  
 A;Note: the list of introns may be incomplete

C;Superfamily: alpha-2-macroglobulin  
 C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein; complement C3b; domain; signal sequence; status predicted <SG>  
 C;PF:1-24/Domain: complement C3 and C3b beta chain #status Predicted <CC3B>>  
 C;PF:1-25-666/Product: complement C3 #status Predicted <CC3>  
 C;PF:1-25-666/671-1663/Product: complement C3 alpha chain #status Predicted <CC3A>  
 C;PF:1-25-666/749-1663/Product: complement C3 alpha chain #status Predicted <CC3B>>  
 C;PF:1-71-1663/Product: complement C3 alpha chain #status Predicted <CC3A>  
 C;PF:671-748/Product: C3a anaphylatoxin #status Predicted <C3T>  
 C;PF:671-748/Product: C3b alpha chain #status Predicted <C3BA>  
 C;PF:946-1103/Product: C3dik fragment #status Predicted <CDK>  
 C;PF:1002-1303/Region: C3d fragment #status Predicted <C3D>>  
 C;PF:1002-1457/Region: properdin binding  
 C;PF:1002-1457/Region: Arg-Ser (C3 convertase) #status Predicted  
 C;PF:1002-1457/Region: carbohydrate (Asn) (covalent) #status Predicted  
 C;PF:1010-1013/Crosslink: thioester (Cys-Gin) #status Predicted  
 C;PF:1130-1304/Cleavage site: Arg-Ser (complement factor I) #status Predicted  
 C;PF:1130-1304/Cleavage site: Arg-Ser (complement factor I) #status Predicted  
 C;PF:1320-1321/Cleavage site: Arg-Ser (complement factor I) #status Predicted

```

Query Match          80.2%; Score 73; DB 1; Length 1663;
Best Local Similarity 75.0%; Pred. No. 0.0017; Gaps 0;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KNRWEDPGKOLYNEA 16
          :|||||: :|||||||
Db       1217 RNRKEEPDQQLYNEA 1232

RESULT 5
C3GP
complement C3 precursor - guinea pig
N/Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-Feb-1992 #sequence revision 07-Oct-1994 #text change 09-Jul-2004
C;Accession: A37156; S031375; D20342; C03342; A31222
C;R/Auerbach, H.S.; Burger, R.; Dodds, A.; Colten, H.R.
A;Title: Molecular basis of complement C3 deficiency in guinea pigs
A;Reference number: MUID:90307998; PMID:1973176
A;Accession: A37156
A;Molecule type: protein
A;Residues: 1-1666 <AUB>
A;Cross-references: UNIPROT:PI12387; UNIPARC:UPI0000127C48; GB:M34054; PMID:911262; PTION:
A;Cross-references: UNIPARC:UPI0000173224
A;Experimental source: complement-activated guinea pig serum
A;Isolated: Form isolated is inactive C3a anaphylatoxin and is missing the carboxyl-terminal
A;Note: Form isolated is inactive C3a anaphylatoxin and is missing the carboxyl-terminal
R;Thomas, M.L.; Tack, B.F.
Biochemistry 22: 942-947, 1983
A;Title: Identification and alignment of a thiol ester site in the third component of guinea pig complement
A;Reference number: A90479; MUID:83178889; PMID:6838833
A;Accession: A20342
A;Molecule type: protein
A;Residues: 676-687 <TH1>
A;Cross-references: UNIPARC:UPI0000173225
A;Accession: D20342
A;Molecule type: protein
A;Residues: 931-1012,1014-1017,'E',1019-1030,'Y' <TH2>
A;Cross-references: UNIPARC:UPI0000173225
A;R/Goldberger, G.; Thomas, M.L.; Tack, B.F.; Williams, J.; Colten, H.R.; Abraham, G.N.

```

J. Biol. Chem. 256, 12617-12619, 1981.  
 A;Title: NH<sub>2</sub>-terminal structure and cleavage of guinea pig pro-C3, the precursor of the alternative complement pathway C3/C5 convertase.  
 A;Reference number: A20342; MURID:82075767; PMID:6458605  
 A;Accession: C20342  
 A;Molecule type: protein  
 A;Residues: 23-38 <SOL>  
 A;Cross-references: UNIPARC:UPI0000173227  
 C;Comment: Complement C3 contains two chains, formed by removal of four residues and linking the amino end of the alternative complement pathway, releases the C3a anaphytoxin and a mediator of inflammation.  
 C;Comment: C3a anaphytoxin is a vasoactive peptide and a mediator of inflammation.  
 C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign particles classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by protease C;Comment: The major site of synthesis of this plasma protein is the liver.  
 C;Superfamily: alpha 2-macroglobulin  
 C;Keywords: acute phase; complement alternate pathway; glycoprotein, F1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-671/Product: complement C3 and C3b beta chain #status predicted <CC3B>  
 F:23-671-676-1666/Product: complement C3 #status predicted <CC3>  
 F:676-1666-Product: complement C3 alpha chain #status predicted <CC3A>  
 F:676-1666-753-Product: C3a anaphytoxin #status predicted <C3T>  
 F:754-1665-Product: complement C3b alpha chain #status predicted <CCBA>  
 F:951-1308-Product: C3d fragment #status predicted <CDK>  
 F:1007-1308-Product: C3d fragment #status predicted <C3D>  
 F:1429-1461/Region: properdin binding  
 F:557-821-630-666-698-725-699-732-712-733-878-1517-1106-1163-1363-1493-1394-1462-1510-1  
 F:753-754/Cleavage site: Arg-Ser (C3 convertase) #status predicted  
 F:944-1620/Binding site: carbonylase (Asn) (covalent) #status predicted  
 F:1015-1018/Cross-link: thioester (Cys-Gln) #status experimental  
 F:1325-1366/Cleavage site: Arg-Ser (complement factor I) #status predicted  
 F:1325-1366/Cleavage site: Arg-Ser (complement factor I) #status predicted

RESULT 6							
Query	KNRWEDEPGKOLYNEV 16	Score 58;	DB 1;	Length 1666;			
Best Local Similarity	63.7%	Pred. No.	0.5;				
Matches	62.5%	Mismatches	4;				
Best Local Similarity	62.5%	Pred. No.	0.5;				
Matches	60.5%	Mismatches	4;				
Query	KNRWEDEPGKOLYNEV 16	Score 52;	DB 2;	Length 1358;			
Best Local Similarity	69.2%	Pred. No.	3.9;				
Matches	69.2%	Mismatches	1;				
Query	KNRWEARQKLYSVEA 1237	Score 52;	DB 3;	Length 11130712			
Best Local Similarity	69.2%	Pred. No.	3.9;				
Matches	69.2%	Mismatches	3;				
Query	RWEDPGKOLYNE 15	Score 52;	DB 4;	Length 94874272;			
Best Local Similarity	69.2%	Pred. No.	3.9;				
Matches	69.2%	Mismatches	0;				
Query	A;Accession: B86241 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1358 <STO> A;Cross references: UNIPROT:Q9SAC6; UNIPARC:UPI0000A10C3; GB:AE005172; NID:94874272; P C;Genetics: A;Map position: 1	Score 52;	DB 5;	Length 5718;			
Best Local Similarity	69.2%	Pred. No.	3.9;				
Matches	69.2%	Mismatches	3;				

Db 223 RWERKGKQMYNPE 235

RESULT 7  
 Db1401  
 Probable selenium-binding protein - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 09-Jul-2004  
 C;Accession: D71401  
 R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzneger, T.; Pohl, T.M.; Terry, N.; Giel avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Funk, B.  
 Nature 391, 485-488, 1998  
 A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Puigdomenech erioff, A.; Moores, T.; Jones, J.D.G.; Enyea, T.; Palme, K.; Benes, V.; Rechman, S.; Ans C.; Chalwatzie, N.  
 A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A;Reference number: A71400; MUID:98121113; PMID:9461215  
 A;Accession: D71401  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Residues: 1-490 <BEV>  
 A;Cross-references: UNIPROT:O23264; UNIPARC:UPI0000000E71; GB:Z97335; NID:g2244747; PID:  
 C;Genetics:

A;Map position: 4COP9-4G3845  
 C;Superfamily: Caenorhabditis elegans hypothetical protein Y37A1B.5  
 Query Match Score 48.9%; Best Local Similarity 56.2%; Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
 Qy 1 KNRWEDEPG-KOLVNVE 15  
 Db 191 KNRNEKPGHSPLYGYD 206

RESULT 8  
 A44068  
 Cell pattern formation-associated protein - *Emmericella nidulans*  
 N;Alternate names: cell differentiation and spatial organization regulator stuA  
 C;Species: *Emmericella nidulans*, *Aspergillus nidulans*  
 C;Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C;Accession: A44068; S27413  
 R;Miller, K.Y.; Wu, J.; Miller, B.L.  
 Genes Dev. 6, 1770-1782, 1992  
 A;Title: StuA is required for cell pattern formation in *Aspergillus*.  
 A;Reference number: A44068; MUID:92387550; PMID:1516832  
 A;Accession: A44068  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-590 <MLL>  
 A;Cross-references: UNIPROT:P36011; UNIPARC:UPI0000136159; EMBL:MS3569; NID:g168095; PID:  
 A;Note: sequence extracted from NCBI backbone (NCBIP:112625)

RESULT 9  
 G82153  
 Hypothetical protein YC1802 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)  
 C;Species: *Vibrio cholerae*  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C;Accession: G82153

RESULT 7  
 Db1401  
 Probable selenium-binding protein - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 09-Jul-2004  
 C;Accession: D71401  
 R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzneger, T.; Pohl, T.M.; Terry, N.; Giel avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Funk, B.  
 Nature 391, 485-488, 1998  
 A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Puigdomenech erioff, A.; Moores, T.; Jones, J.D.G.; Enyea, T.; Palme, K.; Benes, V.; Rechman, S.; Ans C.; Chalwatzie, N.  
 A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A;Reference number: A71400; MUID:98121113; PMID:9461215  
 A;Accession: D71401  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Residues: 1-490 <BEV>  
 A;Cross-references: UNIPROT:O23264; UNIPARC:UPI0000000E71; GB:Z97335; NID:g2244747; PID:  
 C;Genetics:

A;Map position: 4COP9-4G3845  
 C;Superfamily: Caenorhabditis elegans hypothetical protein Y37A1B.5  
 Query Match Score 48.9%; Best Local Similarity 56.2%; Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
 Qy 1 KNRWEDEPG-KOLVNVE 15  
 Db 191 KNRNEKPGHSPLYGYD 206

RESULT 8  
 B07952  
 Pyruvate oxidase (EC 1.2.3.3) [imported] - *Streptococcus pneumoniae* (strain R6)  
 C;Species: *Streptococcus pneumoniae*  
 C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 31-Dec-2004  
 C;Accession: B97952  
 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E., R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAahren, S.; Y., P.; Sun, P.M.; Winkler, M.E.  
 J. Bacteriol. 183, 5709-5717, 2001  
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
 A;Reference number: A97872; MUID:21429245; PMID:11544234  
 A;Accession: B97952  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-591 <UR>  
 A;Cross-references: UNIPROT:QBDQJ4; UNIPARC:UPI00000E34BC; GB:AE007317; PID:AAK99446.1  
 C;Genetics:  
 A;Gene: spxB

RESULT 8  
 A44068  
 Cell pattern formation-associated protein - *Emmericella nidulans*  
 N;Alternate names: cell differentiation and spatial organization regulator stuA  
 C;Species: *Emmericella nidulans*, *Aspergillus nidulans*  
 C;Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C;Accession: A44068; S27413  
 R;Miller, K.Y.; Wu, J.; Miller, B.L.  
 Genes Dev. 6, 1770-1782, 1992  
 A;Title: StuA is required for cell pattern formation in *Aspergillus*.  
 A;Reference number: A44068; MUID:92387550; PMID:1516832  
 A;Accession: A44068  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-590 <MLL>  
 A;Cross-references: UNIPROT:P36011; UNIPARC:UPI0000136159; EMBL:MS3569; NID:g168095; PID:  
 A;Note: sequence extracted from NCBI backbone (NCBIP:112625)

RESULT 9  
 G82153  
 Hypothetical protein YC1802 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)  
 C;Species: *Vibrio cholerae*  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C;Accession: G82153

;Superfamily: thiamine diphosphate-dependent enzyme, acetolactate synthase type  
 ;Keywords: oxidoreductase

	Query Match	Score	DB 2;	Length	591;
Best Local Similarity	47.3%	43;	Pred. No.	47;	
Matches	7;	Conservative	4;	Mismatches	4;
Indels	0;	Gaps	0;		
Y	1 KNRWEDPGKOLYNE 15				
D	475 KNRWEDPGKOLYNE 489				

RESULT 12  
 F95084  
 streptococcus pneumoniae [Imported] - Streptococcus pneumoniae (strain TIGR4)  
 Species: Streptococcus pneumoniae  
 c;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 31-Dec-2004  
 c;Accession: F95084  
 c;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H  
 umayra, J.D.; Holtzman, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf  
 elson, T.; Umayra, E.K.; Holtzman, I.E.  
 c;Science 293: 498-506 ; 2001  
 c;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris  
 et al.;Title: Complete Genome sequence of a virulent isolate of *Streptococcus pneumoniae*.  
 c;Reference number: A95000; MUID:21357209; PMID:11463916  
 c;Accession: F95084  
 c;Status: preliminary  
 c;Molecule type: DNA  
 c;Residues: 1-591 <KUR>  
 c;Cross-references: UNIPROT:Q54970; UNIPARC:UPI000005156C; GB:AE005672; PMID:AAK74871  
 c;Experimental source: strain TIGR4  
 c;Genetics:  
 c;Gene: SP0730  
 c;Superfamily: thiamine diphosphate-dependent enzyme, acetolactate synthase type

	Query	Match	Score	DB	Length	Indels	Gaps	O;
By		Query Match	47.3%	DB 2;	Length 591;			
By		Best Local Similarity	46.7%	Pred. No. 47;				
By		Matches 7;	Conservative	Mismatches 4;				
By	1	KNRWEDPGKOLYNE	15					
By	475	KNKYEDTNKHLFGVD	489					

```

RESULT 13
T12016
Env envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C-Species: human immunodeficiency virus type 1, HIV-1
C-Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #context_change 09-Jul-2004
C-Accesion: T12016
P-McCormchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998.
A-TITLE: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein is
A-Reference number: 9519894
A-Accession: T12016
A-Statutus: preliminary; translated from GB/EMBL/DDJB
A-Molecule type: DNA
A-Residues: 1-852 <MCC>
A-Cross-references: UNIPROT:O41883; UNIPARC:UPI0001081F2; EMBL:U90934; NID:92351783;
A-Genetics:
A-Gene: env
A-Superfamily: type E retrovirus env polyprotein

Query Match Score 43; DB 2; Length 852;
Best Local Similarity 54.5%; Pred. No. 70;
Matches 6; Conservative 3; Mismatches 2; Indels 0;
Gaps 0;

2 NRWDDPGKOLY 12
::: :::

```

90

C3NJ complement C3 precursor - monocled cobra  
 N: Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit  
 C: Species: *Naja naja kaouthia*, *Naja naja siamensis* (monocled cobra)  
 C: Date: 18-Jun-1993 #sequence\_revision 07-Oct-1994 #text\_change 17-Mar-2000  
 C: Accession: A46513  
 R: Fritzinger, D.C.; Petrella, B.C.; Connelly, M.B.; Bredhorst, R.; Vogel, C.W.  
 J: Immunol. 149, 3554-3562, 1992  
 A: Title: Primary structure of cobra complement component C3.  
 A: Reference number: A46513; PMID:93056528; PMID:1431125

Tue May 16 10:49:00 2006

us-09-865-281a-1.rpr

Page 7

Search completed: May 15, 2006, 16:16:59  
Job time : 40 secs

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CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes  
 CC AAB90829 to AAB9241 represent peptides which can be used in the  
 CC exemplification of the present invention.

XX	Sequence 16 AA;	Score 91; DB 4; Length 16;	Best Local Similarity 100.0%; Prod. No. 6.5e-07;	Mismatches 0;	Indels 0;	Gaps 0;
Query Match	100.0%;	Score 91; DB 4; Length 16;	Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;
Best Local Similarity	100.0%;	Score 91; DB 4; Length 16;	Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;
Matches	16;	Score 91; DB 4; Length 16;	Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;
XX	XX	XX	XX	XX	XX	XX
Qy	1 KNRWEDPGKOLYNVEA 16	1 KNRWEDPGKOLYNVEA 16	Qy	1 KNRWEDPGKOLYNVEA 16	1 KNRWEDPGKOLYNVEA 16	Qy
Db	1 KNRWEDPGKOLYNVEA 16	1 KNRWEDPGKOLYNVEA 16	Db	1 KNRWEDPGKOLYNVEA 16	1 KNRWEDPGKOLYNVEA 16	Db
RESULT 3	ADS17594 standard; peptide; 16 AA.	ADS17594 standard; peptide; 16 AA.	RESULT 3	ADS17594 standard; peptide; 16 AA.	ADS17594 standard; peptide; 16 AA.	RESULT 3
ID	ADS17594	ADS17594	ID	ADS17594	ADS17594	ID
XX	XX	XX	XX	XX	XX	XX
AC	ADS17594;	ADS17594;	AC	ADS17594;	ADS17594;	AC
DT	02-DEC-2004 (first entry)	02-DEC-2004 (first entry)	DT	02-DEC-2004 (first entry)	02-DEC-2004 (first entry)	DT
XX	XX	XX	XX	XX	XX	XX
DE	Peptide derived from the C3d peptide and affinity linked to 3H1 antibody.	Peptide derived from the C3d peptide and affinity linked to 3H1 antibody.	DE	Peptide derived from the C3d peptide and affinity linked to 3H1 antibody.	Peptide derived from the C3d peptide and affinity linked to 3H1 antibody.	DE
KW	immunostimulatory; membrane transport; homophilic; signaling protein;	immunostimulatory; membrane transport; homophilic; tumour antigen;	KW	immunostimulatory; membrane transport; homophilic; protein; DNA synthesis; cytoskeletal protein;	immunostimulatory; membrane transport; homophilic; protein; DNA synthesis; cytoskeletal protein;	KW
KW	cespase; kinase; phosphatase; viral protein; nuclear protein; tumour antigen;	nuclear protein; nucleolar protein; viral protein; tumour antigen;	KW	nuclear protein; nucleolar protein; viral protein; tumour antigen;	nuclear protein; nucleolar protein; viral protein; tumour antigen;	KW
KW	cell proliferation; cytoskinesis; membrane transporter peptide;	cell proliferation; cytoskinesis; membrane transporter peptide;	KW	kaposi fibroblast factor; TAT peptide; HIV-1; antennapedia homeodomain;	kaposi fibroblast factor; TAT peptide; HIV-1; antennapedia homeodomain;	KW
KW	herpes virus protein VP22; transporian peptide; Alzheimer's disease;	herpes virus protein VP22; transporian peptide; Alzheimer's disease;	KW	Huntington's disease; Parkinson's disease; C3d; 3H1; monoclonal antibody;	Huntington's disease; Parkinson's disease; C3d; 3H1; monoclonal antibody;	KW
KW	anti-idiotype antibody; carcino-embryonic antigen; CEA;	anti-idiotype antibody; carcino-embryonic antigen; CEA;	KW	anti-idiotype antibody; carcino-embryonic antigen; CEA;	anti-idiotype antibody; carcino-embryonic antigen; CEA;	KW
KW	anti-idiotype vaccine; antibody.	anti-idiotype vaccine; antibody.	KW	anti-idiotype vaccine; antibody.	anti-idiotype vaccine; antibody.	KW
OS	Synthetic.	Synthetic.	OS	Synthetic.	Synthetic.	OS
PN	WO2004078146-A2.	WO2004078146-A2.	PN	WO2004078146-A2.	WO2004078146-A2.	PN
XX	XX	XX	XX	XX	XX	XX
PD	16-SEP-2004.	16-SEP-2004.	PD	16-SEP-2004.	16-SEP-2004.	PD
XX	XX	XX	XX	XX	XX	XX
PF	05-MAR-2004; 2004WO-US006911.	05-MAR-2004; 2004WO-US006911.	PF	05-MAR-2004; 2004WO-US006911.	05-MAR-2004; 2004WO-US006911.	PF
XX	XX	XX	XX	XX	XX	XX
PR	05-MAR-2003; 2003US-0451980P.	05-MAR-2003; 2003US-0451980P.	PR	05-MAR-2003; 2003US-0451980P.	05-MAR-2003; 2003US-0451980P.	PR
XX	XX	XX	XX	XX	XX	XX
PA	(INNE-) INNEXUS BIOTECHNOLOGY INC.	(INNE-) INNEXUS BIOTECHNOLOGY INC.	PA	(INNE-) INNEXUS BIOTECHNOLOGY INC.	(INNE-) INNEXUS BIOTECHNOLOGY INC.	PA
PA	(IMMP-) IMMPhERON INC.	(IMMP-) IMMPhERON INC.	PA	(IMMP-) IMMPhERON INC.	(IMMP-) IMMPhERON INC.	PA
PI	Kohler H, Muller S, Brown TL, Zhao Y, Morgan AC;	Kohler H, Muller S, Brown TL, Zhao Y, Morgan AC;	PI	Kohler H, Muller S, Brown TL, Zhao Y, Morgan AC;	Kohler H, Muller S, Brown TL, Zhao Y, Morgan AC;	PI
XX	XX	XX	XX	XX	XX	XX
DR	WPI; 2004-653567/63.	WPI; 2004-653567/63.	DR	WPI; 2004-653567/63.	WPI; 2004-653567/63.	DR
XX	XX	XX	XX	XX	XX	XX
PT	New compound for regulating normal or infected cell function comprising	New compound for regulating normal or infected cell function comprising	PT	New compound for regulating normal or infected cell function comprising	New compound for regulating normal or infected cell function comprising	PT
PT	an antibody conjugated to a membrane transporter peptide, useful in	an antibody conjugated to a membrane transporter peptide, useful in	PT	an antibody conjugated to a membrane transporter peptide, useful in	an antibody conjugated to a membrane transporter peptide, useful in	PT
PT	preparing a composition for treating or preventing human diseases, e.g.	preparing a composition for treating or preventing human diseases, e.g.	PT	preparing a composition for treating or preventing human diseases, e.g.	preparing a composition for treating or preventing human diseases, e.g.	PT
XX	XX	XX	XX	XX	XX	XX
PS	SEQ ID NO 1; 50PP; English.	SEQ ID NO 1; 50PP; English.	PS	SEQ ID NO 1; 50PP; English.	SEQ ID NO 1; 50PP; English.	PS
XX	The specification describes a fusion protein for regulating normal or	The specification describes a fusion protein for regulating normal or	XX	The specification describes a fusion protein for regulating normal or	The specification describes a fusion protein for regulating normal or	XX
CC	infected cell function, comprising an antibody conjugated to a peptide	infected cell function, comprising an antibody conjugated to a peptide	CC	infected cell function, comprising an antibody conjugated to a peptide	infected cell function, comprising an antibody conjugated to a peptide	CC
CC	having immunostimulatory, membrane transport, and homophilic activities.	having immunostimulatory, membrane transport, and homophilic activities.	CC	having immunostimulatory, membrane transport, and homophilic activities.	having immunostimulatory, membrane transport, and homophilic activities.	CC
CC	The antibody is immunospecific for a signalling protein internal cell	The antibody is immunospecific for a signalling protein internal cell	CC	The antibody is immunospecific for a signalling protein internal cell	The antibody is immunospecific for a signalling protein internal cell	CC
CC	consisting of caspases, kinases or phosphatases, an immature viral	consisting of caspases, kinases or phosphatases, an immature viral	CC	consisting of caspases, kinases or phosphatases, an immature viral	consisting of caspases, kinases or phosphatases, an immature viral	CC
CC	protein, a cell-surface or intracellular tumour antigen, a nuclear or	protein, a cell-surface or intracellular tumour antigen, a nuclear or	CC	protein, a cell-surface or intracellular tumour antigen, a nuclear or	protein, a cell-surface or intracellular tumour antigen, a nuclear or	CC
CC	nucleolar protein participating in regulation of DNA synthesis and gene	nucleolar protein participating in regulation of DNA synthesis and gene	CC	nucleolar protein participating in regulation of DNA synthesis and gene	nucleolar protein participating in regulation of DNA synthesis and gene	CC
CC	expression, or a cytoskeletal protein participating in cell proliferation	expression, or a cytoskeletal protein participating in cell proliferation	CC	expression, or a cytoskeletal protein participating in cell proliferation	expression, or a cytoskeletal protein participating in cell proliferation	CC
CC	or cytostasis. The peptide portion of the fusion protein is preferably a	or cytostasis. The peptide portion of the fusion protein is preferably a	CC	or cytostasis. The peptide portion of the fusion protein is preferably a	or cytostasis. The peptide portion of the fusion protein is preferably a	CC
CC	membrane transporter peptide that is endogenous to kaposi fibroblast	membrane transporter peptide that is endogenous to kaposi fibroblast	CC	membrane transporter peptide that is endogenous to kaposi fibroblast	membrane transporter peptide that is endogenous to kaposi fibroblast	CC
CC	factor, TAT peptides of HIV-1, antennapedia homeodomain-derived peptide,	factor, TAT peptides of HIV-1, antennapedia homeodomain-derived peptide,	CC	factor, TAT peptides of HIV-1, antennapedia homeodomain-derived peptide,	factor, TAT peptides of HIV-1, antennapedia homeodomain-derived peptide,	CC
CC	herpes virus protein VP22, or transportan peptide. Fusion protein of the	herpes virus protein VP22, or transportan peptide. Fusion protein of the	CC	herpes virus protein VP22, or transportan peptide. Fusion protein of the	herpes virus protein VP22, or transportan peptide. Fusion protein of the	CC
CC	invention are useful for preparing a composition for treating or	invention are useful for preparing a composition for treating or	CC	invention are useful for preparing a composition for treating or	invention are useful for preparing a composition for treating or	CC
CC	preventing human diseases, e.g., Alzheimer's disease, Huntington's	preventing human diseases, e.g., Alzheimer's disease, Huntington's	CC	preventing human diseases, e.g., Alzheimer's disease, Huntington's	preventing human diseases, e.g., Alzheimer's disease, Huntington's	CC
CC	disease or Parkinson's disease. The present sequence represents a peptide	disease or Parkinson's disease. The present sequence represents a peptide	CC	disease or Parkinson's disease. The present sequence represents a peptide	disease or Parkinson's disease. The present sequence represents a peptide	CC
CC	derived from the C3d domain of the C3d peptide was affinity cross-linked	derived from the C3d domain of the C3d peptide was affinity cross-linked	CC	derived from the C3d domain of the C3d peptide was affinity cross-linked	derived from the C3d domain of the C3d peptide was affinity cross-linked	CC
CC	with 3H1 monoclonal antibody to produce fusion proteins of the invention.	with 3H1 monoclonal antibody to produce fusion proteins of the invention.	CC	with 3H1 monoclonal antibody to produce fusion proteins of the invention.	with 3H1 monoclonal antibody to produce fusion proteins of the invention.	CC
CC	3H1 is a murine anti-idiotypic antibody which mimics the carcino-	3H1 is a murine anti-idiotypic antibody which mimics the carcino-	CC	3H1 is a murine anti-idiotypic antibody which mimics the carcino-	3H1 is a murine anti-idiotypic antibody which mimics the carcino-	CC
CC	embryonic antigen (CEA), and induces anti-CEA antibodies. The resulting	embryonic antigen (CEA), and induces anti-CEA antibodies. The resulting	CC	embryonic antigen (CEA), and induces anti-CEA antibodies. The resulting	embryonic antigen (CEA), and induces anti-CEA antibodies. The resulting	CC
CC	CD3-3H1 fusion protein was used to enhance an anti-idiotype vaccine.	CD3-3H1 fusion protein was used to enhance an anti-idiotype vaccine.	XX	CD3-3H1 fusion protein was used to enhance an anti-idiotype vaccine.	CD3-3H1 fusion protein was used to enhance an anti-idiotype vaccine.	XX



The invention relates to a multivalent ligand comprising a plurality of signal recognition elements (SRE), binding recognition elements (BRE) and functional elements (FE), and which is bonded to a polymeric scaffold. The SREs are involved, either directly or indirectly, in biological signalling processes, while the BREs facilitate the binding associated with the processes. Examples of SREs used in the multivalent ligand include epitopes (especially one characteristic of a cancer cell), antigens, antibodies or fragments thereof, cell surface receptors, polysaccharides, nucleic acids or small drug-like compounds, and suitable BREs include polysaccharides or metal-chelating groups which are optionally bound to metals. The FE may be a detectable label, a reporter group or an enzyme.

The invention also relates to use of multivalent ligands in a method for inducing a biological response in a biological system such as a cell or organism which comprises one or more receptors recognized by an SRE; a method of enhancing aggregation of biological particles such as cells or viruses using a multivalent ligand complex which comprises several recognition elements which each induce aggregation of one or more of the biological particles; a method for inducing a cellular response or for enhancing cellular response induction using a multivalent ligand; a method of generating an assembly of biological macromolecules or particles by providing a multivalent ligand comprising a molecular scaffold to which several biological macromolecules or particles are attached via BREs, wherein the number, density and spacing of the BREs is controlled; and a library of multivalent ligands of the invention, in which the members of the libraries vary in the type, number and/or relative positioning of recognition elements, the combinations of BREs and SREs present, the presence and/or position of spacers, the number of repeating units or monomers, and the presence, type or number of FEs.

The invention also discloses pharmaceutical compositions comprising multivalent ligands of the invention. The multivalent ligands are useful for modulating immune system cell responses to epitopes, thereby inhibiting or attenuating autoimmune disorders, and are also useful for treating undesired cell proliferation (cancer) and undesired cell migration (metastasis). They can be used in diagnostic applications for the detection of biological molecules or particles in biological systems and are useful for preventing or inhibiting biofouling or removing undesired cells in a selected environment. Sequences ADV42828 ADV42829 represent peptides derived from the complement C3D Peptide of ADV42825 which are attached via a thiol group to a multivalent ligand for the induction of an enhanced immune response.

Q	Sequence 17 AA;	Query Match	100.0%	Score 91;	DB 9;	Length 17;
		Best Local Similarity	100.0%	Pred. No.	6.9e-07;	

Matches	Y	b	16	16	16	16
	1	1	KNRWEDPGKOLYNVEA	KNRWEDPGKOLYNVEA	KNRWEDPGKOLYNVEA	KNRWEDPGKOLYNVEA
16 /	conservative	U;	Mismatches	U;	Indels	U;

**RESULT 6**

DV24828	ADV24828 standard; peptide; 17 AA.
D	ADV24828
X	ADV24828;
X	ADV24828;
X	24-FEB-2005 (first entry)
T	Complement C3d derived peptide, SEQ ID NO:5.
X	Multivalent ligand; cell signaling; diagnostic; decontamination;
X	autoimmune disease; immune disorder; cancer; neoplasm; cancer metastasis;
W	immunosuppressive; immunomodulator; cytostatic; complement C3d.
X	Synthetic.
S	Unidentified.

Qy	1	KNRWEDPGKQLYNVEA 16	Score 91; DB 9; Length 17;	Db	14	KNRWEDEPGKQLYNVEA 29
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Db	2	KNRWEDPGKQLYNVEA 17				
RESULT 7						
ADT92344		standard; peptide; 41 AA.				
ID	ADT92344					
XX						
AC						
XX						
DT	13-JAN-2005	(first entry)				
XX						
DE		Human complement C3 peptide, a marker for colorectal cancer Seq 40.				
XX						
KW		colorectal cancer; quantitative detection assay; protein chip technology;				
XX						
KW		mass spectrometry; Cell proliferation; complement C3.				
XX						
OS		Homo sapiens.				
XX						
PN	WO2004090550-A2.					
XX						
PD	21-OCT-2004.					
XX						
PF	07-APR-2004; 2004WO-DK000263.					
XX						
PR	08-APR-2003; 2003DK-00000541.					
PR	16-JUL-2003; 2003DK-00001055.					
XX						
PA	(COLO-) COLOTECH AS.					
PA	(RASK/) RASKOV H H.					
PI	Raskov HH, Albrethsen J, Gammeltoft S, Bøgebo RM;					
XX						
PR	Diagnosing colorectal cancer in sample from mammal, involves use of marker polypeptides having specific molecular weights and degradation product of human serum albumin.					
PR	XX					
PR	DR; 2004-766501/75.					
PR	XX					
PS	Example 19; SEQ ID NO 40; 132pp; English.					
PS						
XX	This invention relates to a novel method for diagnosing human colorectal cancer using novel protein markers. Specifically it refers to a quantitative detection assay that uses at least one marker chosen from polypeptides having apparent molecular weights ranging between 1005Da and 6680Da, and compares the signal intensity of the marker against a reference value from a healthy person. As such, the present invention describes a method that can be used to diagnose persons with colorectal cancer by means of protein chip technology using mass spectrometry, by identifying differential expression of markers that are indicative of cell proliferation. Preferred protein markers include alpha-fibrinogen protein and human serum albumin where a preferred kit enables detection of a combination of two or more proteins. Accordingly, this method is useful for diagnosing colorectal cancer, as well as predicting clinical outcomes, complications and mortality of an individual already diagnosed with the disease. This peptide sequence is human complement C3 peptide, an down-regulated blood protein marker for colorectal cancer given in an exemplification of the invention.					
XX						
PS	Sequence 41 AA;					
PS						
SQ	Query Match 100.0%; Score 91; DB 8; Length 41;					
Best Local Similarity 100.0%; Pred. No. 1.7e-06;						
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1 KNRWEDPGKQLYNVEA 16					
XX	Sequence 63 AA;					
XX						
Query Match 100.0%; Score 91; DB 5; Length 63;						
Best Local Similarity 100.0%; Pred. No. 2.6e-06;						
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						

Db	9	KNRWEDPGKQLNVEA 24
RESULT 9		
ID	AAU74866	standard; protein; 294 AA.
XX	XX	XX
XX	AAU74858	
AC	AAU74858;	
XX	XX	09-APR-2002 (first entry)
DT	DT	09-APR-2002 (first entry)
XX	XX	Complement pathway protein C3d, N98A mutant.
DE	DE	Complement pathway protein C3d, N98A mutant.
XX	XX	Complement; receptor; CD21; C3d; immune response; B cell stimulator; vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX	XX	Complement pathway protein C3d, R49A mutant.
XX	XX	Complement; receptor; CD21; C3d; immune response; B cell stimulator; vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
OS	OS	Homo sapiens.
OS	OS	Synthetic.
XX	XX	Key
FT	FT	Misc-difference 49 /note= "Wild type Arg substituted by Ala"
XX	XX	Location/Qualifiers
PH	PH	Key
FT	FT	Misc-difference 98 /note= "Wild type Asn substituted by Ala"
XX	XX	Location/Qualifiers
PN	PN	Key
XX	XX	WO200192295-A2.
XX	XX	PR
PD	PD	PN
XX	XX	XX
FT	FT	PD
XX	XX	06-DEC-2001.
XX	XX	30-MAY-2001; 2001WO-CA000785.
XX	XX	PR
PR	PR	PA
XX	XX	(UTOR ) UNIV TORONTO.
PR	PR	XX
XX	XX	30-MAY-2000; 2000US-0207434P.
XX	XX	PA
XX	XX	(UTOR ) UNIV TORONTO.
PA	PA	XX
XX	XX	PT
PI	PI	PI
XX	XX	Isemman DE, Clementza L;
DR	DR	XX
XX	XX	WPI; 2002-114323/15.
PS	PS	PS
XX	XX	Disclosure; Page; 53pp; English.
PT	PT	The invention describes a ligand of the complement receptor 2 (CD21 or
PT	PT	CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
XX	XX	molecule. The ligand is useful in the manufacture of a medicament such as
CC	CC	a vaccine for modulating the immune response of a host (preferably tumour
CC	CC	vaccine), and as antigens in immunogenic compositions, therapeutics
CC	CC	diagnostic reagents, in the generation of diagnostic agents and as cancer
CC	CC	therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC	CC	cells through the CD21/CR19 complex. Non-naturally occurring ligands and
CC	CC	site specific mutated analogues of C3d demonstrate an enhanced binding
CC	CC	affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC	CC	molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC	CC	inducing or enhancing an immune response to an antigen in a host and thus
CC	CC	protects the host against disease caused by the pathogen. This sequence
CC	CC	represents the complement pathway protein C3d N98A mutant, used to study
CC	CC	the interaction of C3d with complement receptor (CD21/CD2), described
CC	CC	in the method of the invention. Note: This sequence does not appear in
CC	CC	the specification but has been created from a C3d wild type sequence
CC	CC	referred on page 11 of the invention
XX	XX	Query Match Score 91; DB 5; Length 294;
SQ	SQ	Best Local Similarity 100.0%; Pred. No. 1.2e-05;
XX	XX	Mismatches 0; Indels 0; Gaps 0;
XX	XX	Score 91; DB 5; Length 294;
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.2e-05;
XX	XX	Mismatches 0; Indels 0; Gaps 0;
Qy	1	KNRWEDPGKQLNVEA 16
Db	224	KNRWEDPGKQLNVEA 239
RESULT 10		
Qy	1	KNRWEDPGKQLNVEA 16
Db	224	KNRWEDPGKQLNVEA 239
RESULT 11		
Qy	1	KNRWEDPGKQLNVEA 16
Db	224	KNRWEDPGKQLNVEA 239
Qy	1	AAU74869
Db	224	AAU74869 standard; protein; 294 AA.
AC	AC	AAU74869;





XX WO200192295-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 30-MAY-2001; 2001WO-CA000785.  
 XX  
 PR 30-MAY-2000; 2000US-0207434P.  
 XX  
 PA (UTOR ) UNIV TORONTO.  
 XX  
 PI Isenman DE, Clementza L;  
 XX DR 2002-114323/15.

PT Ligand useful for modulating immune response such as in the preparation of vaccine comprises CD21 contacting amino acid residues of C3d molecule.

XX Disclosure; Page: 53pp; English.

CC The invention describes a ligand of the complement receptor 2 (CD21 or CD2) comprising amino acid residues 36-39 and 160-167 of the C3d molecule. The ligand is useful in the manufacture of a medicament such as a vaccine for modulating the immune response of a host (preferably tumour vaccine), and as antigens in immunogenic compositions, therapeutics, diagnostic reagents, in the generation of diagnostic agents and as cancer therapeutics. The ligand has the ability to bind CD21 and stimulate B cells through the CD21/CD19 complex. Non-naturally occurring ligands and site specific mutants of C3d demonstrate an enhanced binding affinity for CD21 as compared to the binding affinity of a wild-type C3d molecule. The ligand alters the immunogenicity of an antigen, e.g. by inducing or enhancing an immune response to an antigen in a host and thus protects the host against disease caused by the pathogen. This sequence represents the complement pathway protein C3d E166A mutant, used to study the interaction of C3d with complement receptor 2 (CD21/CD2), described in the method of the invention. Note: This sequence does not appear in the specification but has been created from a C3d wild type sequence referenced on page 11 of the invention

XX Sequence 294 AA;

```
Query Match 100.0%; Score 91; DB 5; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KNRWEDPKQLYNEA 16
      ||||| | | | | |
Db 224 KNRWEDPKQLYNEA 239
```

Search completed: May 15, 2006, 16:12:19
 Job time : 186 secs

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RT	thioester bond.";	Proc. Natl. Acad. Sci. U.S.A. 79:1054-1058(1982).
RN	[6]	PROTEIN SEQUENCE OF 1409-1563; MEDLINE=88154455; PubMed=3279119;
RX		Daoudi M.E.; Becherer J.D.; Lambiris J.D.; RT "A 34-amino acid peptide of the third component of complement mediates RT properdin binding.";
RT		RT J. Immunol. 140:1577-1580(1988).
RN	[7]	STRUCTURE BY NMR OF C3A; RX MEDLINE=88276594; PubMed=3260670;
RX		Nettesheim D.G.; Edalji R.P.; Molaison K.W.; Greer J.; RA Zuideweg E.R.P.; RT "Secondary structure of complement component C3a anaphylatoxin in solution as determined by NMR spectroscopy: differences between crystal and solution conformations.";
RT		RT Proc. Natl. Acad. Sci. U.S.A. 85:5036-5040(1988).
RN	[8]	RPMUTAGENESIS OF THIOESTER BOND REGION.
RX		RA Isaac L.; Iserman D.E.; RT "Structural requirements for thioester bond integrity of complement component C3. Reassessment of the role of thioester bond integrity on the conformation of C3.";
RT		RT Dolmer K.; Sottrup-Jensen L.; RT "Disulfide bridges in human complement component C3b.";
RL	[9]	RL J. Biol. Chem. 267:10062-10069(1992).
RX	DISULFIDE BONDS.	RX MEDLINE=92205653; PubMed=8416818; DOI=10.1016/0014-5793(93)81139-Q;
RA		RA Nagar B.; Jones R.G.; Dieffenbach R.J.; Iserman D.E.; RT Rini J.M.; RT "Disulfide bridges in human complement component C3b.";
RT		RT FEBS Lett. 315:85-90(1993).
RN	CARBOHYDRATE-LINKAGE SITE ASN-85.	RN CARBOHYDRATE-LINKAGE SITE ASN-85.
RX		RX MEDLINE=22660472; PubMed=11274519; DOI=10.1038/nbt827;
RA		RA Zhang H.; Li X.-J.; Martin D.B.; Abersold R.; RT "Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RT		RT RNL Biotechnol. 21:660-666(2003).
RX	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 996-1303.	RX MEDLINE=98259088; PubMed=9596584; DOI=10.1126/science.280.5367.1277;
RA		RA Nagar B.; Jones R.G.; Dieffenbach R.J.; Iserman D.E.; Rini J.M.; RT "X-ray crystal structure of C3d: a C3 fragment and ligand for complement receptor 2".
RT		RT Science 280:1277-1281(1998).
RN	[12]	RN VARIANT C3S ASN-1216.
RX		RX MEDLINE=89309808; PubMed=2473125;
RA	Poznansky M.C.; Cissoid P.M.; Lachmann P.J.; RT "The difference between human C3F and C3S results from a single amino acid change from an asparagine to an aspartate residue at position 1216 on the alpha-chain of the complement component, C3.";	
RT		RT J. Immunol. 143:1254-1258(1989).
RN	[13]	RN ERRATUM, AND RETRACTION.
RX		RX MEDLINE=90063087; PubMed=2584723;
RA	Poznansky M.C.; Cissoid P.M.; Lachmann P.J.;	RA J. Immunol. 143:3860-3862(1989).
RN	[14]	RN VARIANT GLY-10-AND PRO-314.
RX		RX MEDLINE=91011240; PubMed=1976733; DOI=10.1084/jem.172.4.1011;
RA	Bottino M.; Yong Fong K.; So A.K.; Koch C.; Walport M.J.; RT "Molecular basis of polymorphisms of human complement component C3.";	
RL	J. Exp. Med. 172:1011-1017(1990).	RL J. Biol. Chem. 269:28494-28499(1994).
RN	VARIANT C3 DEFICIENCY ASN-549.	RN VARIANT C3 DEFICIENCY ASN-549.
RX		RX MEDLINE=9505640; PubMed=961791;
RA	Singer L.; Whitehead W.T.; Akama H.; Katz Y.; Fishelson Z.; RA Wetsel R.A.; RT "Inherited human complement C3 deficiency. An amino acid substitution in the beta-chain (Asp549 to Asn) impairs C3 secretion.";	
RT		RT J. Biol. Chem. 269:28494-28499(1994).
RL		RL
RN	[16]	RN VARIANT C3 DEFICIENCY GLN-1320.
RP		RP Watanabe Y.; Matsui N.; Kobayashi N.; Kohsaka T.; RA "A novel C3 allotype C3'F02' has an amino acid substitution that may inhibit iC3b synthesis and cause C3-hypocomplementemia.";
RA		RA RT Mol. Immunol. 30:62-67(1993).
RT	-I- FUNCTION: C3 plays a central role in the activation of the complement system. Its processing by C3 convertase is the central reaction in both classical and alternative complement pathways.	CC -I- FUNCTION: Derived from proteolytic degradation of complement C3, C3a anaphylatoxin is a mediator of local inflammatory process. It induces the contraction of smooth muscle, increases vascular permeability and causes histamine release from mast cells and basophilic leukocytes.
CC		CC -I- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg residues, forming two chains, beta and alpha, linked by a disulfide bond. C3 convertase activates C3 by cleaving the alpha chain, releasing C3a anaphylatoxin and generating C3b (beta chain + alpha' chain). During pregnancy, C3dg exists as a complex (probably a 2:2:2 heterohexamer) with AGT and the proform of PRG2.
CC		CC -I- PTM: C3b is rapidly split in two positions by Factor I and a cofactor to form iC3b (inactivated C3b) and C3f which is released. Then iC3b is slowly cleaved (possibly by Factor I) to form C3c and C3dg. Other proteases produce other fragments such as C3d or C3g.
CC		CC -I- POLYMORPHISM: There are two alleles: C3S (C3 slow), the most common allele in all races and C3F (C3 fast), relatively rare in Caucasoids, less common in Black Americans, extremely rare in Orientals.
CC		CC -I- DISEASE: Defects in C3 are the cause of C3 deficiency [MIM:120700]. It can result in susceptibility to pyrogenic infection.
CC		CC -I- SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC		CC -I- SIMILARITY: Contains 1 NTR domain.
CC		CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC		CC EMBL; K02765; AAA85332; 1; mRNA.
DR		DR EMBL; AY513239; AAR89061; 1; Genomic_DNA.
DR		DR PIR; A94065; C3HU.
DR		DR PDB; 1C3D; X-ray; @=;
DR		DR PDB; 1GHQ; X-ray; @=;
DR		DR GlycoSwitchDB; P01024;
DR		DR SWISS-2DPAGE; P01024;
DR		DR Sifera-2DPAGE; P01024;
DR		DR Ensembl; ENSG00000125730; Homo_sapiens.
DR		DR HGNC; HGNC:1318; C3.
DR		DR MTM; 120700;
DR		DR GO; GO:0005102; P:receptor binding; TAS.
DR		DR GO; GO:0006985; P:immune response; TAS.
DR		DR InterPro; IPR011626; A2M_comp.
DR		DR InterPro; IPR002830; A2M_N.
DR		DR InterPro; IPR011625; A2M_N_2.
DR		DR InterPro; IPR000020; Anaphylatoxin.
DR		DR InterPro; IPR001840; Anaphylatoxin.
DR		DR InterPro; IPR001539; Macroglobulina2.
DR		DR InterPro; IPR001134; Netrin_C.
DR		DR Pfam; PF00207; A2M; 1.
DR		DR Pfam; PF07678; A2M_comp; 1.
DR		DR Pfam; PF07705; A2M_N_2; 1.
DR		DR Pfam; PF07677; A2M_recep; 1.
DR		DR Pfam; PF01823; ANATO; 1.
DR		DR Pfam; PF01759; NTR; 1.

DR	PRINTS;	PR0004; ANAPHYLATOXIN.
DR	ProDom;	PD003264; Anaphylatoxin; 1.
DR	ProDom;	PD003264; Anaphylatoxin; 1.
Qy	1 KNRWEDPGKQLYNEA 16	Query Match 100.0%; Score 91; DB 1; Length 1663; Best Local Similarity 100.0%; Pred. No. 2.8e-06; Matches 16; Conservatism 0; Mismatches 0; Indels 0; Gaps 0;
Db	1217 KNRWEDPGKQLYNEA 1232	
<b>RESULT 2</b>		
	CO3 RAT	STANDARD;
	ID CO3 RAT	PRT; 1663 AA.
	AC P01026;	
	DT 21-JUL-1986 (Rel. 01, Created)	
	DT 01-AUG-1990 (Rel. 15, Last sequence update)	
	DT 13-SEP-2005 (Rel. 48, Last annotation update)	
	DE Complement C3 precursor [Contains: Complement C3 beta chain; Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha chain].	
	GN Name=C3;	
	RS Rattus norvegicus (Rat).	
	OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii;	
	OC Muridae; Muridae; Murinae; Rattus.	
	OX NCBI_TAXID=10116;	
	RN [1]	
	RP NUCLEOTIDE SEQUENCE.	
	RC STRAIN=Wistar; TISSUE=Liver;	
	RX MEDLINE=90245672; PubMed=2236397;	
	MSIumi Y.; Sohda M.; Ikehara Y.; Daniels J.S.; Daughaday W.H.; Bradshaw R.A.; "Purification, characterization, and amino acid sequence of rat complement C3.";	
	RA RT Nucleic Acids Res. 18:2178-2178(1990). [2]	
	RN PROTEIN SEQUENCE OF 671-748.	
	RX MEDLINE=79062262; PubMed=309768;	
	JA Jacobs J.W.; Rubin J.S.; Hugli T.E.; Bogardt R.A. Jr., Mariz I.K., "Estrogen regulation of tissue-specific expression of complement C3.";	
	RA RA Dittlie C.R.; Sundstrom S.A.; Komm B.S., Ponce-De-Leon H., Yi Z., Teuscher C., "Function: C3 plays a central role in the activation of the complement system. Its processing by C3 convertase is the central reaction in both classical and alternative complement pathways. After activation C3b can bind covalently, via its reactive thiolesser, to cell surface carbohydrates or immune aggregates.	
	RL J. Biol. Chem. 264:1691-16947(1989).	
	CC CC - FUNCTION: Derived from proteolytic degradation of complement C3, C3a anaphylatoxin is mediator of local inflammatory process. It induces the contraction of smooth muscle, increases vascular permeability and causes histamine release from mast cells and basophilic leukocytes.	
	CC CC - SUBUNIT: C3 precursor is first processed by the removal of 4 Arg residues, forming two chains, beta and alpha, linked by a disulfide bond. C3 convertase activates C3 by cleaving the alpha chain, releasing C3a anaphylatoxin and generating C3b (beta chain + alpha chain).	
	CC CC - SIMILARITY: Contains 1 anaphylatoxin-like domain.	
	CC CC - SIMILARITY: Contains 1 NTR domain.	
	CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is removed.	

			removed.
FT	TURN	1114	1115
FT	STRAND	1118	1118
FT	HELIX	1127	1134
FT	TURN	1137	1138
FT	HELIX	1139	1158
FT	TURN	1159	1161
FT	TURN	1163	1164
FT	HELIX	1165	1180
FT	TURN	1181	1182
FT	HELIX	1186	1198
FT	TURN	1199	1200
FT	TURN	1204	1205
FT	HELIX	1205	1213
FT	STRAND	1215	1215
FT	TURN	1218	1218
FT	STRAND	1219	1219
FT	TURN	1223	1224
FT	HELIX	1226	1242
FT	TURN	1243	1244
FT	TURN	1246	1247
FT	HELIX	1249	1258
FT	TURN	1263	1264
FT	TURN	1266	1267
FT	HELIX	1269	1285
SQ	SEQUENCE	1663 AA:	186460 MW: 2F87CCB143CDD4BC CRC64;
Query Match	Best Local Similarity	87.9%	Score 80; DB 1; Length 1653;
Matches	13; Conservative	81.2%	Pred. No. 0.00023; Mismatches 0; Indels 0; Gaps 0;
Db	1217 RNRWEEPGQQLYNEA 16	1217 RNRWEEPGQQLYNEA 1232	
Qy	1 KNRWEDPGKOLYNEA 16		
Db	1217 RNRWEEPGQQLYNEA 1232		
<b>RESULT 3</b>			
CO3 - RABBIT	CO3 - RABBIT	STANDARD:	PRT: 726 AA.
AC	AC		
DT	01-OCT-1989 (Rel. 1.2, Created)		
DT	01-OCT-1989 (Rel. 1.2, Last sequence update)		
DT	10-MAY-2005 (Rel. 4.7, Last annotation update)		
DB	Complement C3 alpha chain (Fragment).		
GN	Name=C3;		
OS	Oryctolagus cuniculus (Rabbit)		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae; Oryctolagus.		
NCBI_TaxID	9986;		
OX	[1]		
RP	NUCLEOTIDE SEQUENCE		
RX	MedlineB@06307; PubMed=3019881;		
RA	Kusano M., Choi N.H., Tomita M., Yamamoto K., Migita S., Sekiya T., Nishimura S.;		
RT	"Nucleotide sequence of cDNA and derived amino acid sequence of rabbit complement component C3 alpha-chain.";		
RL	Immunol. Invest. 15:365-378(1986).		
CC	-I- FUNCTION: C3 plays a central role in the activation of the complement system. Its processing by C3 convertase is the central reaction in both classical and alternative complement pathways.		
CC	After activation C3b can bind covalently, via its reactive thioester, to cell surface carbohydrates or immune aggregates.		
CC	-I- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg residues, forming two chains, beta and alpha, linked by a disulfide bond. C3 convertase activates C3 by cleaving the alpha chain, releasing C3a anaphylatoxin and generating C3b (beta chain + alpha, chain).		
CC	-I- SIMILARITY: Contains 1 NTR domain.		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not		
CC	removed.		
CC	CC		
DR	EMBL; M32431; AAA31190.1; -; mRNA.		
DR	PTR; A27602; A27602.		
DR	HSSP; P01024; 1C5D.		
DR	SMR; P12247; 58-162.		
DR	InterPro; IPR011626; A2M comp.		
DR	InterPro; IPR011627; A2M receptor.		
DR	InterPro; IPR00020; Anaphylatoxin.		
DR	InterPro; IPR001599; MacroglobulinA2.		
DR	InterPro; IPR001134; Netrin C.		
PFam	PF0678; A2M comp; 1.		
DR	PFam; PF07677; A2M receptor.		
PFam	PF01759; NTR; 1.		
DR	PROSITE; PS00477; ALPH1 2 MACROGLOBULIN; 1.		
DR	PROSITE; PS01177; ANAPHYLATOXIN 1; PARTIAL.		
DR	PROSITE; PS01178; ANAPHYLATOXIN 2; PARTIAL.		
DR	PROSITE; PS01189; NTR; 1.		
KW	Complement alternate pathway; Complement pathway; Glycoprotein; Immune response; Inflammatory response; Innate immunity; Plasma		
KW	Tioster ester bond.		
KW	Complement C3 alpha chain.		
FT	CHAIN <1		
FT	DOMAIN 581	726	NTR
FT	N-linked (GlcNAc. . )	724	(Potential).
FT	CARBOHYD 2	233	N-linked (GlcNAc. . )
FT	CARBOHYD 233	233	(Potential).
FT	CARBOHYD 680	680	N-linked (GlcNAc. . )
FT	CROSSLINK 73	76	Isoglutamyl cysteine thioester (Cys-Gln).
FT	NON_TER 1	1	
SQ	SEQUENCE 726 AA; 81844 MW; F4B4C35D461300E9 CRC64;		
Query	Match 86.8%; Score 79; DB 1; Length 726;		
Matches	13; Conservatve 3; Mismatches 0; Indels 0; Gaps 0;		
Db	1 KNRWEDPGKOLYNEA 16 280 KNRWEEPGQQLYNEA 295		
<b>RESULT 4</b>			
O46544_SHEEP	NUCLEOTIDE SEQUENCE		
ID	O46544_SHEEP PRELIMINARY; PRT; 349 AA.		
AC	O46544_		
DT	01-JUN-1998 (TREMBLref). 06, Created)		
DT	01-JUN-1998 (TREMBLref). 06, Last sequence update)		
DT	01-OCT-2003 (TREMBLref). 25, Last annotation update)		
DE	Complement component C3 (Fragment).		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Laurasatheria; Cetartiodactyla; Ruminantia; Peccidae; Bovidae; Caprinae; Ovis.		
NCBI_TaxID	9940;		
OX	NCBI_TaxID=9940;		
RN			
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=white laine; TISSUE=Liver;		
RX	"Ubiquitination and dimerization of complement receptor type 2 on sheep B cells.";		
RA	Hein W.R., Duddler L., Marston W.L., Landsverk T., Young A.J., Avila D.;		
RA	Pubmed=98309471; Pubmed=967256.		
RT	"Ubiquitination and dimerization of complement receptor type 2 on sheep B cells.";		
RT	J. Immunol. 161:458-466 (1998).		
RL	EMBL; AF038130; AAB92374.2; -; mRNA.		
DR	HSSP; P01026; 100F.		
DR	SMR; O46544; 19-322.		
DR	GO; GO:00486; F: endopeptidase inhibitor activity; IEA.		
DR	InterPro; IPR011626; A2M comp.		
DR	InterPro; IPR001599; MacroglobulinA2.		
DR	PFam; PF0678; A2M comp; 1.		
DR	PROSITE; PS00477; ALPH1 2 MACROGLOBULIN; 1.		
FT	NON_TER 1	1	
FT	349 AA; 39679 MW; 70C2023E42ED5EE3 CRC64;		
SQ	SEQUENCE 349 AA; 39679 MW;		

Query Match	84.6%	Score 77; DB 2; Length 349;						
Best Local Similarity	81.2%	Pred. No. 0_00013;						
Matches 13;	Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;			
Qy	1 KNRWEDPGKOLYNEA 16							
Db	241 KNRWEEPNKKLYNVEA 256							
RESULT 5								
Q29289_IG	Q29289_PIG PRELIMINARY;	PRT;	154 AA.					
AC	Q29289_							
DT	01-OCT-1996 (TREMBLrel. 01. Created)							
DT	01-NOV-1996 (TREMBLrel. 01. Last sequence update)							
DE	Complement C3 (Fragment).							
OS	Sus scrofa (Pig).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.							
OC	NCBI_TaxID=9823;							
OX	RN							
RP	NUCLEOTIDE SEQUENCE.							
RC	TISSUE=Small intestine;							
RX	MBELINE=6321607; PubMed=8672129; DOI=10.1007/s003359900153;							
RA	Winterer A.K., Fredholm M., Davies W.;							
RR	"Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones.,"							
RT	Mamm. Genome 7:509-517(1996).							
RL	EMBL; F14640; CA23173.1; -; mRNA.							
DR	EMBL; P01026; 1QOF.							
DR	SNR; Q29289_8-91.							
DR	InterPro; IPR011626; A2M_comp.							
DR	Pfam; PF07678; A2M_comp_1.							
FT	NON_TER 1							
FT	NON_TER 154 AA; 154							
SQ	SEQUENCE 154 AA; 17440 MW;	6DC7661C1253ED45 CRC64;						
Query Match	83.5%	Score 76; DB 2; Length 154;						
Best Local Similarity	75.0%	Pred. No. 7-de-05;						
Matches 12;	Conservative	4;	Mismatches 0;	Indels 0;	Gaps 0;			
Qy	1 KNRWEDPGKOLYNEA 16							
Db	10 RNRWEEPNQKLKNVEA 25							
RESULT 6								
Q9Z115_MESAU	Q9Z115_MESAU PRELIMINARY;	PRT;	310 AA.					
AC	Q9Z115_							
DT	01-MAY-1999 (TREMBLrel. 10. Created)							
DT	01-MAY-1999 (TREMBLrel. 10. Last sequence update)							
DE	Complement C3 (Fragment).							
OS	Mesocricetus auratus (Golden hamster).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.							
OC	NCBI_TaxID=10036;							
OX	RN							
RP	NUCLEOTIDE SEQUENCE.							
RA	Yamamoto K., Inoue N., Sakiyama H.;							
RU	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.							
DR	EMBL; AB024455; BAA75923.1; -; mRNA.							
DR	HSSP; P01026; 1QOF.							
DR	SNR; Q9Z115_18-293.							
DR	GO; GO:004866; Fendopeptidase inhibitor activity; IEA.							
DR	InterPro; IPR011626; A2M_comp.							
DR	InterPro; IPR001599; MacrofogloblnA2.							
DR	Pfam; PF07678; A2M_comp_1.							
PROSITE; PS00477; ALPHA_2_MACROGLOBULIN_1.								
Query Match	80.2%	Score 73; DB 2; Length 303;						
Best Local Similarity	75.0%	Pred. No. 0.0056;						
Matches 12;	Conservative	3;	Mismatches 1;	Indels 0;	Gaps 0;			
Qy	1 KNRWEDPGKOLYNEA 16							
Db	10 RNRWEEPNQKLKNVEA 25							
RESULT 8								
C03_MOUSE	C03_MOUSE STANDARD;	PRT;	1663 AA.					
ID	C03_MOUSE							
AC	P01027_	061370_						
DT	21-JUL-1986 (Rel. 01. Created)							
DT	01-FEB-1996 (Rel. 33. Last sequence update)							
DE	Complement C3 precursor (HSE-NSF) Icontains: Complement C3 beta chain; Complement C3 alpha chain; C3a anaphylatoxin; Complement C3dg fragment; Complement C3c fragment; Complement C3g fragment; Complement C3f fragment; Complement C3d fragment; Complement C3 fragment; Complement C3f fragment.							
DE	Name=C3;							
OS	Mus musculus (Mouse).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi; Muridae; Muridae; Muridae; Murinae; Mus.							
OC	NCBI_TaxID=10090;							
RN	NUCLEOTIDE SEQUENCE (ISOFORM LONG).							
RX	MEDLINE=85038854; PubMed=6208565;							

RA	Fey G.H., Lundwall A., Wetzel R.A., Tack B.F., de Brujin M.H.L., Domdey H.; "Nucleotide sequence of complement protein C3."; RT	RX MEDLINE=95053742; PubMed=7964485; DOI=10.1084/jem.180.6.2079;
RA	"Structure of murine complement component C3. I. Nucleotide sequence of cloned complementary and genomic DNA coding for the beta chain."; [3]	RX MEDLINE=65054818; PubMed=6548745;
RA	Lundwall A., Wetzel R.A., Domdey H., Tack B.F., Fey G.H., "Structure of murine complement component C3. I. Nucleotide sequence of cloned complementary and genomic DNA coding for the beta chain."; [3]	RX MEDLINE=65113177; PubMed=2578664;
RA	Sottrup-Jensen L., Stepanik T.M., Kristensen T., Lonblad P.B., Jones C.M., Wierzbicki D.M., Magnusson S., Domdey H., Wetzel R.A., Lundwall A., Tack B.F., Fey G.H.; "Common evolutionary origin of alpha 2-macroglobulin and complement components C3 and C4"; Proc. Natl. Acad. Sci. U.S.A. 82:9-13 (1985).	RX MEDLINE=65113177; PubMed=2578664;
RA	[4]	RX MEDLINE=64045420; PubMed=6345427; DOI=10.1007/BF00205869;
RA	FEY G., Domdey H., Wiebauer K., Whitehead A.S., Odink K.; RT "Structure and expression of the C3 gene"; Springer Semin. Immunopathol. 6:119-14 (1983).	RX MEDLINE=64045420; PubMed=6345427;
RA	[5]	RX MEDLINE=65054519; PubMed=6094532;
RA	NUCLEOTIDE SEQUENCE OF 671-1663 (ISOFORM LONG); Domdey H., Lundwall A., Davidson F., Gibson T., Tack B.F., Fey G.H.; "Structure of murine complement component C3. II. Nucleotide sequence of cloned complementary DNA coding for the alpha chain."; J. Biol. Chem. 259:13857-13862 (1984).	RX MEDLINE=65054519; PubMed=6094532;
RA	[6]	RX MEDLINE=63117730; PubMed=6961437;
RA	Domdey H., Wiebauer K., Kazmaier M., Mueller V., Odink K., Fey G.H.; "Characterization of the mRNA and cloned cDNA specifying the third component of mouse complement."; Proc. Natl. Acad. Sci. U.S.A. 79:7619-7623 (1982).	RX MEDLINE=63117730; PubMed=6961437;
RA	[7]	RX MEDLINE=64201365; PubMed=6603661;
RA	NUCLEOTIDE SEQUENCE OF 658-761; Domdey H., Wiebauer K., Domdey H.; "Amino acid sequences of mouse complement C3 derived from nucleotide sequences of cloned cDNA."; Ann. N. Y. Acad. Sci. 421:307-312 (1983).	RX MEDLINE=64201365; PubMed=6603661;
RA	[8]	RX MEDLINE=93117622; PubMed=6985498;
RA	Wiebauer K., Domdey H., Diggelmann H., Fey G.; "Isolation and analysis of genomic DNA clones encoding the third component of mouse complement."; Proc. Natl. Acad. Sci. U.S.A. 79:7077-7081 (1982).	RX MEDLINE=93117622; PubMed=6985498;
RA	[9]	RX PROTEIN SEQUENCE OF 25-41 AND 749-760.
RA	Hamaida J.-I., Cavanaugh P.G., Miki K., Nicolson G.L.; "A paracrine migration-stimulating factor for metastatic tumor cells secreted by mouse hepatic sinusoidal endothelial cells: identification as complement component C3b"; Cancer Res. 53:4418-4423 (1993).	RX MEDLINE=9373334; PubMed=836938;
RA	Sato T., Hong M.H., Jin C.H., Ishimi Y., Udagawa N., Shinkai T., Abe E., Suda T.; "The specific production of the third component of complement by osteoblastic cells treated with 1 alpha,25-dihydroxyvitamin D3."; FEBS Lett. 285:21-24 (1991).	RX MEDLINE=91293104; PubMed=2063778; DOI=10.1016/0014-5793(91)80715-F;
RA	[10]	RX PROTEIN SEQUENCE OF 25-31 AND 671-680.
RA	Hamada J.-I., Cavanaugh P.G., Miki K., Nicolson G.L.; "A paracrine migration-stimulating factor for metastatic tumor cells secreted by mouse hepatic sinusoidal endothelial cells: identification as complement component C3b"; Cancer Res. 53:4418-4423 (1993).	RX MEDLINE=91293104; PubMed=2063778; DOI=10.1016/0014-5793(91)80715-F;
RA	[11]	RX PROTEIN SEQUENCE OF 25-31 AND 671-680.
RA	ALTERNATIVE INITIATION.	RX PROSITE; PS01177; ANAPHYLATOXIN_1;
RA		RX PROSITE; PS01178; ANAPHYLATOXIN_2;





DR	InterPro; IPR001840; Anaphylatoxin.	GN	ORFNames=T16B5_10;
DR	IPR001599; Macroglobina2.	OS	Arabidopsis; <i>Thaliana</i> (Mouse-ear cress). Embryophyta; Tracheophyta;
DR	InterPro; IPR001134; Netrin_C.	OC	Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
DR	Pfam; PF00207; A2M; 1.	OC	NCBI_TaxID=3702;
DR	Pfam; PF07678; A2M_comp; 1.	OX	[1]
DR	Pfam; PF01835; A2M_N; 1.	RN	NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, SUBCELLULAR LOCATION, RP DEVELOPMENTAL STAGE, AND MUTAGENESIS OF GLY-1268.
DR	Pfam; PF07703; A2M_N_2; 1.	RP	MEDLINE=21380420; PubMed=11487701; DOI=10.1105/tpc.13.8.1907;
DR	Pfam; PF007677; A2M_recep; 1.	RX	Yu T.-S., Kofler H., Haenauer R.E., Hiller D., Fluegge U.-I., Zeeman S.C., Smith A.M., Rossmann J., Lloyd J., Steup M., Lue W.-L., Chen J., Weber A.; "The Arabidopsis <i>sex1</i> mutant is defective in the R1 protein, a general regulator of starch degradation in plants, and not in the chloroplast hexose transporter".
DR	Pfam; PF01821; ANATO; 1.	RA	Plant Cell 13:1907-1918 (2001).
DR	PRINTS; PR00004; ANAPHYLATOXIN.	RN	[2]
DR	ProDom; PD003264; Anaphylatoxin; 1.	RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
DR	PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.	RC	STRAIN=cu. Columbia;
DR	PROSITE; PS01177; ANAPHYLATOXIN_1; 1.	RX	MEDLINE=21016719; PubMed=11130712; DOI=10.1088/35048500;
DR	PROSITE; PS01178; ANAPHYLATOXIN_2; 1.	RA	Theologis A., Baker J.R., Palm C.J., Feddersen N.A., Kaul S., Buehler E., Alonso J., Altai H., Arsuaga R., Bowman C.L., Brooks S.Y., Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K., Dunn P., Eguil P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.P., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenevskaya I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luos J.S., Maiti R., Marzali A., Miltitzer J., Miranda M., Nguyen M., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo P., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shih P., Southwick A.M., Sun H., Tallon L.J., Tambang G., Toriumi M.J., Town C.D., Utterback T., van Aken S., Vayberg M., Vysotskaya V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> ."; Nature 408:816-820 (2000).
FT	SIGNAL 1 22	RN	[3]
FT	CHAIN 23 1666	RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 12220-1399.
FT	CHAIN 23 671	RC	STRAIN=cu. Columbia;
FT	CHAIN 676 1666	RX	MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
FT	PEPTIDE 676 753	RA	Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Cheuk R.F., Southwick A.M., Wu H.C., Kim C.J., Wu T., Yu G., Karlin-Newman G., Liu S.X., Lam B., Sakano H., Chang C.H., Lee J.M., Miranda M., Quach H.L., Tripp M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Chan M.M., Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.P., Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M., Khan S., Koescema E., Ishikada J., Jiang P.X., Jones T., Kawai J., Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Empirical analysis of transcriptional activity in the <i>Arabidopsis genome</i> "; RT
FT	CHAIN 754 1666	RN	Science 302:842-846 (2003).
FT	CHAIN 993 1666	CC	-!- FUNCTION: Mediates the incorporation of phosphate into starch-like alpha-Glucan + phosphate.
FT	DOMAIN 698 733	CC	-!- COFACTOR: Magnesium (By similarity).
FT	DOMAIN 1522 1664	CC	-!- SUBCELLULAR LOCATION: Chloroplast; starch granules.
FT	COMBPIAS 672 675	CC	-!- DEVELOPMENTAL STAGE: The level of protein does not vary in a circadian rhythm and is stable throughout day and night (at protein level).
FT	COMBPIAS 1242 1248	CC	-!- SIMILARITY: Belongs to the PEP-utilizing enzyme family.
FT	SITE 753 754	CC	-!- CAUTION: Ref. 2 sequence differs from that shown due to erroneous gene model prediction.
FT	SITE 992 993	CC	
FT	CARBOHYD 944 944	CC	
FT	CARBOHYD 1620 1620	CC	
FT	DISULFID 557 821	CC	
FT	DISULFID 630 666	CC	
FT	DISULFID 698 725	CC	
FT	DISULFID 699 732	CC	
FT	DISULFID 712 733	CC	
FT	DISULFID 878 1517	CC	
FT	DISULFID 1106 1163	CC	
FT	DISULFID 1363 1493	CC	
FT	DISULFID 1394 1462	CC	
FT	DISULFID 1510 1515	CC	
FT	DISULFID 1522 1593	CC	
FT	DISULFID 1540 1664	CC	
FT	DISULFID 1640 1649	CC	
FT	CROSSLINK 1015 1018	CC	
FT	CROSSLINK 731 731	CC	
FT	CONFLICT 1018 1018	CC	
FT	CONFLICT 1018 1018	CC	
FT	SEQUENCE 1666 AA 186488 MW; 1C1F1219344AF049 CRC64;	CC	
Query Match	Best Local Similarity 63.7%	Score 58; DB 1; Length 1666;	RT
Matches 10;	Conservative	Indels 0; Gaps 0;	RT
Sequence	1666 AA;		RT
Qy	1 KNRMEDPGKOLYNVEA 16		RU
Db	1222 KNRWEEARQKLYSVEA 1237		CC
RESULT 12			CC
R1_ARATH	STANDARD; PRT; 1399 AA.		CC
ID	RL ARATH Q93V00; Q9PPB2; 01-FEB-2005 (Rel. 46, Created)		CC
AC	Q93V00; Q9PPB2; 01-FEB-2005 (Rel. 46, Last sequence update)		CC
DT	13-SEP-2005 (Rel. 48, Last annotation update)		CC
DE	Alpha-glucan water dikinase, chloroplast precursor (EC 2.7.9.4)		CC
DB	(Search-related RI protein) (Starch excess protein 1).		CC
GN	Name=SEX1; Synonyms=R1; OrderedLocusNames=At1g0760;		CC

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CC	EMBL; AC007354; AAD31337..1; ALI SEQ; Genomic_DNA.
CC	EMBL; AF372893; AAK49609..1; ALT INIT; mRNA.
CC	EMBL; AY057722; AAL15352..1; ALT INIT; mRNA.
CC	PIR; BB6241..BB6241; PEP mobile.
CC	InterPro; IPR002879.. PEP utilized.
CC	InterPro; IPR001021.. PEP_UTILIZERS.
CC	InterPro; IPR002192.. PPDK_PEP_bd.
CC	PROSITE; PS000742.. PEP_ENYMES_2; FALSE NEG.
CC	PROSITE; PS00370.. PEP_ENYMES_PHOS SITE; FALSE NEG.
CC	KW ATP-binding; Carbohydrate metabolism; Chloroplast; Kinase; Nucleotide-binding; Phosphorylation; Transerase; Transcriptase; Peptide.
CC	FT TRANSIT 1 75 Chloroplast (By similarity).
CC	FT CHAIN 76 1399 Alpha-Glucan water dikinase.
CC	ACT_SITE 1004 1004 tele-phosphotididine intermediate (By similarity).
CC	PT MOD RES 1004 1004 Phosphohistidine (By similarity).
CC	PT MUTAGEN 1268 1268 G>E: In sex-1; induces an excess of starch in leaves after a long period of darkness.
CC	SQ SEQUENCE 1399 AA; 156582 MW; 1FEF285376B479EB CRC64;
Query Match 57.1% Score 52; DB 1; Length 1399;	
Best Local Similarity 69.2%; Pred. No. 14; Gaps 0;	
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
Qy 3 RWEDEPGKGOLYNVE 15	
Db 223 RWERKGKQMYNPE 235	
RESULT 13 09SGX4_ARATH PRELIMINARY; PRT; 1540 AA.	
ID Q9SGX4_ARATH PRELIMINARY;	
AC Q9SGX4;	
DT 01-MAY-2000 (TREMBLref).	13, Created)
DT 01-MAY-2000 (TREMBLref).	13, Last sequence update)
DT 01-MAR-2004 (TREMBLref).	26, Last annotation update)
DE F20B24_19	
OS Arabidopsis thaliana (Mouse-ear cress).	
OC Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;	
OC Spermatophota; Magnoliophyta; eudicotyledons; core eudicots; rosids;	
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.	
NCBI_TaxID=3702;	
[1]	
RN NUCLEOTIDE SEQUENCE.	
RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Khan C., Kim C., Altefa H., Bei Q., Chin C., Chou J., Choi E., Conn L., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharshy N., Nguyen M., Nguyen M., Palme C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., RA Toriumi M., Vaysberg M., Yu G., Federer Spiel N.A., Theologis A., Ecker J.R., RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.	
[2]	
RN NUCLEOTIDE SEQUENCE.	
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shin P., Altafa H., Bei B., Chin C., Choi J., Choi E., Conn L., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharshy N., Nguyen M., Nguyen M., Palme C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., RA Toriumi M., Vaysberg M., Yu G., Davis R., Federer Spiel N.A., Theologis A., Ecker J., RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	
RL	

AC Q9MZA7;  
 DR 01-OCT-2000 (TREMBLrel. 15; Created)  
 DR 01-OCT-2000 (TREMBLrel. 15; Last sequence update)  
 DR 01-JUN-2003 (TREMBLrel. 24; Last annotation update)  
 DB MHC class I antigen (Fragment).  
 GN Name=Bain-US\*L13;  
 OS Barbus intermedius (Lake tana barbels).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Barbus.  
 RN NCBI\_TaxID=40831;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kruiswijk C.P.; Stet R.J.M.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR AJ007997; CAB97341.1; -; Genomic\_DNA.  
 DR HSSP; P01897; LDP.  
 DR GO; GO:0042612; CMHC class I protein complex; IEA.  
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
 DR GO; GO:0019882; B:antigen presentation; IEA.  
 DR InterPro; IPR001039; MHC\_I\_alpha\_A1A2.  
 DR Pfam; PF00129; MHC\_I\_1.  
 DR PRINTS; PRO1638; MHCCASSI.  
 FT NON\_TER 1 1  
 FT NON\_TER 92 92  
 SQ SEQUENCE 92 AA; 10463 MW; A1D08F030F9E144 CRC64;

Query Match 54.9%; Score 50; DB 2; Length 92;  
 Best Local Similarity 50.0%; Pred. No. 1.5;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KNKWDPEPKQLYNEA 16  
 Db 53 KNKWDPEPKQLYNEA 68

Search completed: May 15, 2006, 16:16:15  
 Job time : 231 secs

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OM protein - protein search, using SW model

Run on: May 15, 2006, 16:28:51 ; Search time 180 Seconds  
(without alignments)  
39.056 Million cell updates/sec

Title: US-09-865-281A-1  
Perfect score: 91  
Sequence: 1 KNRWEDPGKOLYNVEA 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1: geneseqP1980s:\*

2: geneseqP1990s:\*

3: geneseqP2000s:\*

4: geneseqP2001s:\*

5: geneseqP2002s:\*

6: geneseqP2003as:\*

7: geneseqP2003bs:\*

8: geneseqP2004as:\*

9: geneseqP2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	91	100.0	16	4	AAB23360	Aab92360 Miscellaneous
2	91	100.0	16	6	ABP5217	Abp58217 Immunost
3	91	100.0	16	8	ADS17594	Peptide d
4	91	100.0	16	8	ADY24825	Ad24825 CR2 bindi
5	38	41.8	16	2	AAW2826	Aaw32826 HIV-1 CDC
6	37	40.7	16	1	AAPB2479	Aap82479 Peptide c
7	37	40.7	16	2	AAR24424	Aar24424 Sequence
8	37	40.7	16	2	AAR85369	Aaa85369 HTLV-IIIB
9	37	40.7	16	2	AAW07391	Aaw07391 HIV-1 CD4
10	37	40.7	16	2	AAW10345	HIV epitope
11	37	40.7	16	2	AAW16512	HTLV-IIIB
12	37	40.7	16	2	AAW12824	HIV-1 SC
13	37	40.7	16	2	AAW16535	HIV-1 BH1
14	37	40.7	16	2	AAW32825	Aaw32825 HIV-1 SP2
15	37	40.7	16	2	AAW32822	Aaw32822 HIV-1 BRU
16	37	40.7	16	2	AAW32823	Aaw32823 HIV-1 MN
17	37	40.7	16	2	AAW32828	Aaw32828 HIV-1 RF
18	37	40.7	16	2	AAW5140	Aaw53140 HIV Sp160
19	37	40.7	16	2	AAB85381	Heier T-
20	37	40.7	16	2	AAW76982	Aaw76982 fusion im
21	37	40.7	16	2	AAW51937	Aaw51937 HIV Sp120
22	37	40.7	16	2	AAY04046	Aay04046 Covalent
23	37	40.7	16	3	AAY73159	Aay73159 HIV-deriv
24	37	40.7	16	4	AAB49073	Aab49073 HIV gp120

#### ALIGNMENTS

RESULT 1  
AAB92360  
ID AAB92360 standard; peptide; 16 AA.

XX AC AAB92360;

XX DT 22-JUN-2001 (first entry)

XX DE Miscellaneous peptide SEQ ID NO:1536.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;

KW blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX PN WO2000059900-A2.

XX XX PD 23-NOV-2000.

XX XX PP 17-MAY-2000; 2000WO-US013576.  
XX PR 17-MAY-1999; 99US-0134406P.  
PR 10-SEP-1999; 99US-0153406P.  
PR 15-OCT-1999; 99US-0159783P.  
XX PA (CONJ-) CONJUCHEM INC.  
XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
XX XX Disclosure; Page 707; 7339PP; English.  
XX PD WPI; 2001-112059/12.

XX The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (II) and a reactive group (III) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/chiol groups on blood components to form a peptide stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic



Sequence 16 AA;

Query Match 100.0%; Score 91; DR 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16  
DB 1 KNRWEDPGKQLYNVEA 16

**RESULT 4**  
ID ADV24825 standard; peptide; 16 AA.  
XX  
AC ADV24825;  
XX DT 24-FEB-2005 (first entry)  
XX DE CR2-binding complement C3d peptide, SEQ ID NO:2.  
XX KW Multivalent ligand; cell signaling; diagnostic; decontamination;  
KW autoimmune disease; immune disorder; cancer; neoplasm; cancer metastasis;  
KW immunosuppressive; immunomodulator; cytostatic; complement C3d.  
OS Unidentified.  
XX PN US200448801-A1.  
XX PD 09-DEC-2004.  
XX PF 22-MAR-2004; 2004US-00806056.  
XX PR 21-MAR-2000; 2000US-0191014P.  
PR 21-MAR-2001; 2001US-00815296.  
PR 21-MAR-2003; 2003US-0456778P.  
XX PA (KIESL) KIESSLING L L.  
PA (GRIF/) GRIFFITH B R.  
PA (GSTF/) GESTWICKI J E.  
PA (STRO/) STRONG L.  
XX PI Kiessling LL, Griffith BR, Gestwicki JE, Strong L;  
DR WPI; 2005-046763/05.  
XX PR Novel multivalent ligand, useful for inducing biological response,  
PR enhancing aggregation of biological particles and enhancing induction of  
cellular response.  
XX PS Example 3; SEQ ID NO 2; 76pp; English.  
XX The invention relates to a multivalent ligand comprising a plurality of  
CC signal recognition elements (SRE), bonding recognition elements (BRE) and  
functional elements (FE), and which is bonded to a polymeric scaffold.  
CC The SREs are involved, either directly or indirectly, in biological  
CC signalling processes, while the BREs facilitate the binding associated  
with the process. Examples of SREs used in the multivalent ligand include  
CC epitopes (especially one characteristic of cancer cell), antigens,  
CC antibodies or fragments thereof, cell surface receptors, polysaccharides,  
CC nucleic acids or small drug-like compounds, and suitable BREs include  
CC polysaccharides or metal-chelating groups which are optionally bound to  
CC metals. The FE may be a detectable label, a reporter group or an enzyme.  
CC The invention also relates to use of multivalent ligands in a method for  
CC inducing a biological response in a biological system such as a cell or  
CC organism which comprises one or more receptors recognized by an SRE; a  
CC method of enhancing aggregation of biological particles such as cells or  
CC viruses using a multivalent ligand complex which comprises several  
CC recognition elements which each induce aggregation of one or more of the  
CC biological particles; a method for inducing a cellular response or for  
CC enhancing cellular response induction using a multivalent ligand; a  
CC method of generating an assembly of biological macromolecules or  
CC particles by providing a multivalent ligand comprising a molecular

Sequence 16 AA;

Query Match 100.0%; Score 91; DR 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KNRWEDPGKQLYNVEA 16  
Db 1 KNRWEDPGKQLYNVEA 16

**RESULT 5**  
ID AAW32826 standard; peptide; 16 AA.  
XX AAW32826;  
AC AAW32826;  
XX DT 17-OCT-2003 (revised)  
DT 14-JAN-1998 (first entry)  
XX HIV-1 CDC4 envelope glycoprotein 120 T cell epitope T1.  
DE HIV-1  
XX KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;  
KW recognition; B lymphocyte; type specific; antibody; vaccine; protection;  
KW immune response; infection; neutralisation; epitope.  
XX Human immunodeficiency virus 1.  
OS WO9714436-A1.  
PN XX  
XX 24-APR-1997.  
XX PT 96WO-US016911.  
PT 18-OCT-1996;  
XX PR 95US-00546515.  
PR 20-OCT-1995;  
PR 09-FEB-1996;  
XX PA (YDU-) UNIV DUKE.  
XX Haynes BF, Parker TJ;  
XX DR WPI; 1997-244862/22.  
XX PS Disclosure; Page 23; 104pp; English.  
XX An essentially pure hydrophilic peptide, comprising at least 1 antigenic  
CC determinant of human immunodeficiency virus (HIV) envelope (env)  
CC glycoprotein (gp) recognised by B lymphocytes, when covalently linked to  
CC a carrier molecule, i.e. the present sequence, induces the production of

CC high titres of protective, type specific anti-HIV antibodies (Ab) in a  
 CC mammal. The peptide can be used in vaccines for producing a protective  
 CC immune response to HIV infection, while a HIV neutralising Ab can be  
 CC induced in a primate by administering a composition comprising HIV env  
 CC peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to  
 CC standardise OS field)

XX Sequence 16 AA;

Query Match	41.8%	Score 38;	DB 2;	Length 16;	
Best Local Similarity	54.5%	Pred. No.	96;		
Matches	2;	Mismatches	3;	Indels	0;
		OS		Gaps	0;

Qy            2 NRWEDPGKQLY 12  
 Db            5 NRWQVQGKAMY 15

RESULT 6  
 1D AAP82479 standard; protein; 16 AA.  
 XX  
 AC AAP82479;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 12-NOV-1990 (first entry)  
 XX Peptide component of AIDS vaccine.  
 DE AIDS vaccine; T-cells.  
 KW AIDS vaccine; T-cells.  
 OS Synthetic.  
 XX EP273716-A.  
 XX PD 06-JUL-1988.  
 XX PF 23-DEC-1987; 87EP-00311391.  
 XX PR 30-DEC-1986; 86US-00947935.  
 PR 12-FEB-1987; 87US-0014430.  
 XX PA (USDC ) US SEC OF COMMERCE.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
 PI Delisi C, Margalit H, Cornette JL, Ouyang CS;  
 DR WPI; 1988-184640/27.  
 XX  
 PT Synthetic peptide(s) as vaccines for AIDS - selected from peptide regions  
 PT which can fold as a maximally amphipathic helix recognised by T cells.  
 XX  
 PS Claim 9; Page 10; 16pp; English.  
 XX  
 CC This peptide is a component of an AIDS vaccine. It can fold as a  
 CC maximally amphipathic helix and is recognised by T-cells immune to the  
 CC AIDS virus envelope protein. See also AAP82462-78. (Updated on 25-MAR-  
 CC 2003 to correct PA field.)  
 XX Sequence 16 AA;

Query Match	40.7%	Score 37;	DB 1;	Length 16;	
Best Local Similarity	45.5%	Pred. No.	1.4e+02;		
Matches	5;	Mismatches	3;	Indels	0;
		OS		Gaps	0;

Qy            2 NRWEDPGKQLY 12  
 Db            5 NMWQEVGKAMY 15

RESULT 7  
 1D AAR24424 standard; peptide; 16 AA.

XX AAR24424;  
 AC XX DT 25-MAR-2003 (revised)  
 XX DT 21-NOV-1992 (first entry)  
 XX DE Sequence of T helper peptide of gp120 at amino acid residue numbers 105-  
 DE 117(T2).  
 XX Vaccine; AIDS; HIV-1; carrier peptide.  
 XX Homo sapiens.  
 XX PN WO9208491-A1.  
 XX PD 29-MAY-1992.  
 XX PF 19-NOV-1991; 91WO-US008653.  
 XX PR 20-NOV-1990; 90US-00616247.  
 XX PA (TANO-) TANOX BIOSYSTEMS INC.  
 XX  
 PI Chang TW, Fung MSC;  
 XX DR WPI; 1992-19955/24.  
 XX PT Vaccines comprising anti-idiotype antibody conjugates - induce prodn. of  
 PT neutralising antibodies against HIV-1 for immunisation against HIV  
 PT infection and AIDS.  
 XX  
 PS Claim 12; Page 26 and page 15; 29pp; English.  
 XX  
 CC The invention includes epitope-directed immunization with a vaccine in  
 CC which an anti-idiotype antibody is conjugated to a carrier, which can be  
 CC either a protein or its derived T helper peptide. The carrier is one  
 CC against which the vaccine recipient has previously immunized or otherwise  
 CC previously exposed, or which enhances the immune response against the  
 CC anti-idiotype antibody. One exemplary anti-idiotype antibody which  
 CC induces antibodies against the PND is AB19-4. Where the anti-idiotype  
 CC induces Ab3 against HIV-1, the carrier preferably is HBsAg or HIV-1 p24,  
 CC or peptide f either HBsAg or HIV-1 p24 including a T helper  
 CC determinant. "PND" = the principal neutralizing determinant ("PND") of  
 CC gp120. A T helper peptide with the sequence in AAR24423, or immunological  
 CC equivalents of this sequence is suitable for conjugation with AB19-4 or  
 CC other anti-idiotypes which induce Ab3 against HIV-1. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX Sequence 16 AA;  
 XX  
 Query Match 40.7%; Score 37; DB 2; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 Qy            2 NRWEDPGKQLY 12  
 Db            6 NMWQEVGKAMY 16

RESULT 8  
 1D AAR85369 standard; peptide; 16 AA.

XX AAR85369;  
 AC XX DT 16-OCT-2003 (revised)  
 DT 12-JUN-1996 (first entry)  
 XX DE HTLV-IIIB gp120 envelope T cell epitope T1.  
 XX Human immunodeficiency virus; HIV; HTLV-IIIB; envelope; glycoprotein;  
 KW hydrophilic; immunisation; antibody production; fusion peptide; SP-10;  
 KW conjugate; carrier.

PT from HIV env protein.  
 XX  
 OS Human immunodeficiency virus 1.  
 PS WO9529700-A1.  
 PN XX  
 PD 09-NOV-1995.  
 PR XX  
 PT 28-APR-1995; 95WO-US005465.  
 PT XX  
 PR 29-APR-1994; 94US-00235305.  
 PA XX  
 (UYDU-) UNIV DUKE.  
 PA XX  
 PI Haynes BF, Parker TJ;  
 XX DR WPI: 1995-392926/50.  
 PT New peptide(s) corresponding to HIV sequences - used for inducing protective immunity to HIV and in the treatment of e.g. auto-immune disease, infectious disease or tumours.  
 XX PS Claim 6; Page 16; 128pp; English.  
 XX  
 CC ARR85169 and ARR85370 are HTLV-IIIB gp120 envelope T cell epitopes T1 and T2. The two peptides correspond to amino acids 428-443 and 112-124 of the HIV isolate, HTLV-IIIB gp120 envelope protein. The peptides can be conjugated to SP-10 and "SP-10-like" regions of other HIV isolates. Conjugates produced are capable of inducing the production of high titres of protective, type-specific, anti-HIV antibodies. Helper T cells and cytotoxic T cells are also activated by the peptide immunogens. (updated on 16-OCT-2003 to standardise OS field)  
 XX SQ Sequence 16 AA;  
 Query Match 40.7%; Score 37; DB 2; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 1.e+02;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 NRWEDPGKQLY 12  
 Db 5 NMWQEVGKAMY 15

RESULT 10  
 AAW10345 ID AAW10345 standard; peptide; 16 AA.  
 AC AAW10345;  
 AC DT 15-OCT-1997 (first entry)  
 DE HIV epitope env T1 amino acid residues 428-443 of gp120.  
 KW Human immunodeficiency virus type-1; HIV-1; T cell response; detection; peripheral blood mononuclear cell; PBMC.  
 XX  
 KW KW  
 XX Synthetic.  
 OS PN WOS641189-A1.  
 XX PD 19-DEC-1996.  
 XX PF 07-JUN-1996;  
 XX PR 07-JUN-1995;  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PI Shearer GM, Berzofsky JA, Clerici M;  
 DR WPI: 1997-108658/10.  
 XX  
 PT Diagnosis of exposure to infectious agents, partic. HIV - by detecting activation of peripheral blood mononuclear cells from patient by epitope of infectious agent.  
 XX  
 PS Claim 15; Page 62; 82pp; English.  
 XX  
 CC The present sequence represents a synthetic HIV-1 gp120 peptide env T1 for use in a method for diagnosing exposure of a patient to human immunodeficiency virus (HIV). The method involves: (a) obtaining peripheral blood mononuclear cells (PBMC) from a patient; (b) incubating the PBMC with at least 1 synthetic peptide representing an epitope(s) of the infectious agent (e.g. the present sequence); and (c) determining the activation of the PBMC as a result of the incubation in step (b). The method can provide for the early detection of exposure to infectious organisms, specifically HIV in this case. The method can be used to assess exposure to HIV without concomitant infection. It also provides an earlier identification of HIV exposure, than is provided by seroconversion  
 XX Sequence 16 AA;  
 SQ Sequence 16 AA;

RESULT 9  
 AAW07391 ID AAW07391 standard; peptide; 16 AA.  
 AC AAW07391;  
 DT 16-OCT-2003 (revised)  
 DT 24-FEB-1997 (first entry)  
 XX  
 DE HIV-1 CD4 binding site.  
 KW HIV-1; gp120; V3 loop; common consensus PND domain; envelop; CD4; binding site; stem-loop; lysine branched peptide; AIDS.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX JP08231423-A.  
 PN XX  
 PD 10-SEP-1996.  
 PR XX  
 PF 27-FEB-1995; 95JP-00038835.  
 PR XX  
 PA (TERU ) TERUMO CORP.  
 PA (OKUD/) OKUDA K.  
 XX  
 DR WPI: 1996-461278/46.  
 XX  
 PT Novel AIDS Vaccine - Comprises branched lysine peptide fragments derived

Query Match Best Local Similarity Matches	40.7%; 5;	Score 37; DB 2; Length 16; Pred: No. 1.4e+02; Mismatches 3; Indels 0; Gaps 0;	DT 17-OCT-2003 (revised) DT 14-JAN-1998 (first entry)
Qy	2 NRWEDPGKQLY 12  :: : 5 NMWQEVGKAMY 15	KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp; KW recognition; B lymphocyte; type specific; antibody; vaccine; protection; KW immune response; infection; neutralisation; epitope.	XX HIV-1 SC envelope glycoprotein 120 T cell epitope T1. XX DE XX KW XX KW XX KW XX OS Human immunodeficiency virus 1. XX XX WO9714436-A1.
Db	AAW16512 ID AAW16512 standard; peptide; 16 AA. AC AAW16512; XX DT 14-JAN-1998 (first entry) XX DE HTLV-IIIB envelope glycoprotein 120 T cell epitope T1. XX KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp; KW recognition; B lymphocyte; type specific; antibody; vaccine; protection; KW immune response; infection; neutralisation; epitope. XX OS Human lymphotropic virus. XX PN WO9714436-A1. XX PD 24-APR-1997. XX PF 18-OCT-1996; 96WO-US016911. XX PR 20-OCT-1995; 95US-00546515. XX PR 09-FEB-1996; 96US-00599266. XX (UYDU-) UNIV DUKE. XX Haynes BF, Palmer TJ; XX WPI; 1997-244862/22. XX Disclosure; Page 23; 104pp; English. XX PT Synthetic human immunodeficiency virus vaccine - comprising hydrophilic peptide corresponding to at least 1 antigenic determinant of envelope glyco:protein recognised by B lymphocytes. XX PS Disclosure; Page 23; 104pp; English. XX PT XX CC An essentially pure hydrophilic peptide, comprising at least 1 antigenic determinant of human immunodeficiency virus (HIV) envelope (env) glycoprotein (gp) recognised by B lymphocytes, when covalently linked to a carrier molecule, i.e. the present sequence, induces the production of high titres of protective, type specific anti-HIV antibodies (Ab) in a mammal. The peptide can be used in vaccines for producing a protective immune response to HIV infection, while a HIV neutralising Ab can be induced in a primate by administering a composition comprising HIV env glyco:protein peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to standardise OS field) XX SQ Sequence 16 AA; XX Query Match Score 37; DB 2; Length 16; CC Best Local Similarity 45.5%; Pred: No. 1.4e+02; CC Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0; CC Indels 0; Gaps 0; CC Qy 2 NRWEDPGKQLY 12 CC  :: : CC 5 NMWQEVGKAMY 15 CC Db DE HIV-1 BH10 envelope glycoprotein 120 T cell epitope T1. CC XX HIV-1 BH10 envelope glycoprotein 120 T cell epitope T1. CC XX DE CC XX KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp; CC KW recognition; B lymphocyte; type specific; antibody; vaccine; protection; CC KW immune response; infection; neutralisation; epitope. CC XX OS Human immunodeficiency virus 1. CC XX PN WO9714436-A1. CC XX		
RESULT 11	AAW16535 ID AAW16535 standard; peptide; 16 AA.	AAW16535 AC AAW16535; XX DT 17-OCT-2003 (revised) XX DT 14-JAN-1998 (first entry)	RESULT 12 AAW12824 ID AAW12824 standard; peptide; 16 AA. AC AAW12824; XX AC AAW12824; XX PN WO9714436-A1.

PD 24-APR-1997. PT Synthetic human immunodeficiency virus vaccine - comprising hydrophilic  
 XX peptide corresponding to at least 1 antigenic determinant of envelope  
 PF 18-OCT-1996; PT glyco-protein recognised by B lymphocytes.  
 XX  
 PR 96WO-US016911. XX  
 PR 20-OCT-1995; PS Disclosure; Page 23; 104pp; English.  
 95US-00546515. XX  
 PR 09-FEB-1996; PS  
 XX (UYDU-) UNIV DUKE. XX  
 PA An essentially pure hydrophilic peptide, comprising at least 1 antigenic  
 XX determinant of human immunodeficiency virus (HIV) envelope (env)  
 CC glycoprotein (gp) recognised by B lymphocytes, when covalently linked to  
 CC a carrier molecule, i.e. the present sequence, induces the production of  
 CC high titres of protective, type specific anti-HIV antibodies (Ab) in a  
 CC mammal. The peptide can be used in vaccines for producing a protective  
 CC immune response to HIV infection, while a HIV neutralising Ab can be  
 CC induced in a primate by administering a composition comprising HIV env  
 CC peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to  
 CC standardise OS field)  
 XX  
 PS Sequence 16 AA;  
 XX  
 Query Match Score 37; DB 2; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 NRWEDPGKOLY 12  
 | :| :| :| :| :|  
 Db 5 NMWQEVGKAMY 15  
 XX  
 RESULT 15  
 AAW32822 ID AAW32822 standard; peptide; 16 AA.  
 XX  
 AC AAW32822;  
 XX  
 Query Match Score 37; DB 2; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 NRWEDPGKOLY 12  
 | :| :| :| :|  
 Db 5 NMWQEVGKAMY 15  
 XX  
 RESULT 14  
 AAW32825 ID AAW32825 standard; peptide; 16 AA.  
 XX  
 AC AAW32825;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 14-JAN-1998 (first entry)  
 XX  
 DE HIV-1 SF2 envelope glycoprotein 120 T cell epitope T1.  
 XX  
 KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;  
 KW recognition; B lymphocyte; type specific; antibody; vaccine; protection;  
 KW immune response; infection; neutralisation; epitope.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO9714436-A1.  
 XX  
 PR 24-APR-1997.  
 XX  
 PR 18-OCT-1996; 96WO-US016911.  
 XX  
 PR 20-OCT-1995; 95US-00546515.  
 XX  
 PR 09-FEB-1996; 96US-00599266.  
 XX (UYDU-) UNIV DUKE.  
 PA Haynes BF, Parker TJ,  
 XX  
 DR WPI; 1997-244862/22.  
 XX  
 PS Disclosure; Page 23; 104pp; English.  
 XX  
 PR Synthetic human immunodeficiency virus vaccine - comprising at least 1 antigenic  
 XX peptide corresponding to at least 1 antigenic determinant of envelope  
 PT glycoprotein (gp) recognised by B lymphocytes, when covalently linked to  
 CC a carrier molecule, i.e. the present sequence, induces the production of  
 CC high titres of protective, type specific anti-HIV antibodies (Ab) in a  
 CC mammal. The peptide can be used in vaccines for producing a protective  
 CC immune response to HIV infection, while a HIV neutralising Ab can be  
 XX

CC induced in a primate by administering a composition comprising HIV env  
CC peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to  
CC standardise OS field)

XX

SQ Sequence 16 AA:

Query Match	40.7%	Score 37;	DB 2;	Length 16;
Best Local Similarity	45.5%	Pred. No.	1.4e+02;	
Matches	5;	Mismatches	3;	Indels 0;
Conservative				Gaps 0;

Qy 2 NRWEDPGKQLY 12  
|::|:  
Db 5 NMWQEVGKAMY 15

Search completed: May 15, 2006, 16:34:34

Job time : 182 secs

GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd.						
MM protein - protein search, using sw model						
run on:	May 15, 2006, 16:39:16 ; Search time 45 Seconds (without alignments) 29.396 Million cell up					
title:	US-09-865-281A-1					
perfect score:	91					
sequence:	1 KNRWEDPGKOLYNVEA 16					
scoring table:	BLOSUM62					
searched:	Gapop 10.0 , Gapext 0.5					
Total number of hits satisfying chosen parameters:	572060 seqs, 82675679 residues					
minimum DB seq length:	16					
maximum DB seq length:	16					
post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
database :	Issued Patents AA:*					
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being analysed and is derived by analysis of the total score distribution	7712					
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result No.	Score	Query Match Length	DB ID	Description		
1	91	100 0	16 2	US-09-070-907-1	Sequ	
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4	37	40 7	16 1	US-08-213-124-5	Sequ	
5	37	40 7	16 1	US-08-488-252-35	Sequ	
6	37	40 7	16 1	US-07-847-311A-15	Sequ	
7	37	40 7	16 2	US-09-046-373-1	Sequ	
8	37	40 7	16 2	US-09-53-230	Sequ	
9	37	40 7	16 2	US-09-340-798A-40	Sequ	
10	37	40 7	16 2	US-09-311-784A-308	Sequ	
11	37	40 7	16 2	US-09-724-961-51	Sequ	
12	37	40 7	16 2	US-09-580-018-51	Sequ	
13	37	40 7	16 2	US-09-724-551-51	Sequ	
14	37	40 7	16 2	US-09-862-849-1	Sequ	
15	37	40 7	16 2	US-10-114-716A-1	Sequ	
16	37	40 7	16 2	US-09-724-953-9	Sequ	
17	37	40 7	16 2	US-09-724-967-9	Sequ	
18	37	40 7	16 2	US-09-724-940-51	Sequ	
19	37	40 7	16 2	US-09-979-952-9	Sequ	
20	37	40 7	16 2	US-09-585-17-9	Sequ	
21	31.9	31.9	16 1	US-08-257-528B-22	Sequ	
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23	31.9	31.9	16 1	US-08-463-566A-22	Sequ	
24	29	31.9	16 1	US-08-465-217A-22	Sequ	
25	29	31.9	16 1	US-08-464-329A-22	Sequ	
26	29	31.9	16 1	US-08-467-881A-22	Sequ	
27	29	31.9	16 1	US-08-468-507A-22	Sequ	

**RESULT 1**  
US-09-010-907-1  
; Sequence 1, Application US/09070907  
; Patent No. 6238667  
; GENERAL INFORMATION:  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: METHOD OF AFFINITY CROSS-LINKING BIOLOGICALLY ACTIVE  
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES TO ANTIBODIES.  
; FILE REFERENCE: 35629  
; CURRENT APPLICATION NUMBER: US/09/070,907  
; CURRENT FILING DATE: 1998-05-04  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AMINO ACID  
; OTHER INFORMATION: SEQUENCE DERIVED FROM Cd3 peptide  
US-09-070-907-1

Query Match      100.0% ; Score 91; DB 2; Length 16;  
Best Local Similarity      100.0% ; Pred. No. 7,4e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy	1 KNRWEDPGKOLYNEA 16
Db	1 KNRWEDPGKOLYNEA 16

**RESULT 2**  
US-09-673-548A-1516  
; Sequence 1536, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: ConjuChem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudreau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623, 548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134, 406  
; PRIOR FILING DATE: 1999-05-17

PRIOR APPLICATION NUMBER: 60/153,406  
 PRIOR FILING DATE: 1999-09-10  
 PRIOR APPLICATION NUMBER: 60/159,783  
 PRIOR FILING DATE: 1999-10-18  
 NUMBER OF SEQ ID NOS: 1617  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1536  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-623-548A-1536

Query Match 100.0%; Score 91; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKOLYNEA 16  
 Db 1 KNRWEDPGKOLYNEA 16

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RESULT 3  
 US-09-657-276-1536  
 Sequence 1536, Application US/09657276  
 Patent No. 6887470  
 GENERAL INFORMATION:  
 APPLICANT: ConjuChem, Inc.  
 BRIDON, Alan  
 Ezrin, Dominique  
 Peter  
 Holmes, Darren  
 Miller, Peter  
 APPLICANT: Thibaudeau, Karen  
 TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
 PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
 TITLE OF INVENTION: COMPONENTS  
 FILE REFERENCE: 2110  
 CURRENT APPLICATION NUMBER: US/09/657,276  
 CURRENT FILING DATE: 2000-09-07  
 PRIOR APPLICATION NUMBER: 60/134,406  
 PRIOR FILING DATE: 1999-05-17  
 PRIOR APPLICATION NUMBER: 60/153,406  
 PRIOR FILING DATE: 1999-09-10  
 PRIOR APPLICATION NUMBER: 60/159,783  
 PRIOR FILING DATE: 1999-10-18  
 NUMBER OF SEQ ID NOS: 1617  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1536  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-657-276-1536

Query Match 100.0%; Score 91; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
 US-09-213-124-5  
 Sequence 5, Application US/08213124  
 Patent No. 5693325  
 GENERAL INFORMATION:  
 APPLICANT: Kahn, Michael

APPLICATION NUMBER: 08\326,676  
 FILING DATE: 07-Jun-1995  
 APPLICATION NUMBER: 07\26,605  
 FILING DATE: 09-July-1991  
 APPLICATION NUMBER: 07\63,262  
 FILING DATE: 01-Mar-1991  
 APPLICATION NUMBER: 07\55,321  
 FILING DATE: 12-Feb-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Maria C. H. Lin  
 REGISTRATION NUMBER: 29,323  
 REFERENCE/DOCKET NUMBER: 1151-4004 USA  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: (212) 758-4800  
 TOPOLOGY: Unknown  
 US-08-488-252-35

Query Match Score 37; DB 1; Length 16;  
 Best Local Similarity 45.5%; Prod. No. 11;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 6  
 US-07-847-311A-15  
 Sequence 15, Application US/07847311A  
 GENERAL INFORMATION:  
 APPLICANT: Berzofsky, Jay A.  
 APPLICANT: Takesita, Toshiyuki  
 APPLICANT: Shirai, Mutsunori  
 APPLICANT: Pendleton, C.D.  
 APPLICANT: Koslowski, Steven  
 APPLICANT: Margulies, David H.  
 TITLE OF INVENTION: Potent Peptide for Stimulation of Cytotoxic T Lymphocytes Specific for the HIV-I Envelope  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Birch, Stewart, Kolash & Birch  
 STREET: 301 N. Washington  
 CITY: Falls Church  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 22046-0747

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/847,311A  
 FILING DATE: 06-MAR-1992  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svensson, Leonard R.  
 REGISTRATION NUMBER: 30,330  
 REFERENCE/DOCKET NUMBER: 1173-392P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-241-1300  
 TELEX: 703-241-2848  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 amino acids

Query Match Score 37; DB 1; Length 16;  
 Best Local Similarity 45.5%; Prod. No. 11;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 OTHER INFORMATION: /label= peptide  
 OTHER INFORMATION: /note= "peptide TI, T-cell helper determinant in HIV-I envelope glycoproteins"  
 OTHER INFORMATION: HIV-I envelope glycoprotein  
 US-07-847-311A-15

Query Match Score 37; DB 1; Length 16;  
 Best Local Similarity 45.5%; Prod. No. 11;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 OTHER INFORMATION: /label= peptide  
 OTHER INFORMATION: /note= "peptide TI, T-cell helper determinant in HIV-I envelope glycoproteins"  
 OTHER INFORMATION: HIV-I envelope glycoprotein  
 US-09-046-373-1  
 Sequence 1, Application US/09046373  
 Patent No. 6225714  
 GENERAL INFORMATION:  
 APPLICANT: Sudhir Paul  
 APPLICANT: Larry J. Smith  
 APPLICANT: Gennady Golobov  
 TITLE OF INVENTION: Methods for Identifying Inducers and Inhibitors of Catalytic Antibodies, Compositions and Their Use  
 FILE REFERENCE: UNMC 63123  
 CURRENT APPLICATION NUMBER: US/09/046,373  
 CURRENT FILING DATE: 1998-03-23  
 NUMBER OF SEQ ID NOS: 10  
 SEQ ID NO 1  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Human Immunodeficiency Virus-1  
 US-09-046-373-1

Query Match Score 37; DB 2; Length 16;  
 Best Local Similarity 45.5%; Prod. No. 11;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 OTHER INFORMATION: /label= peptide  
 OTHER INFORMATION: /note= "peptide TI, T-cell helper determinant in HIV-I envelope glycoproteins"  
 OTHER INFORMATION: HIV-I envelope glycoprotein  
 US-09-046-373-1  
 Sequence 1, Application US/09046373  
 Patent No. 6413517  
 GENERAL INFORMATION:  
 APPLICANT: Sette, Alessandro  
 TITLE OF INVENTION: Identification of Broadly Reactive DR Restricted Epitopes  
 NUMBER OF SEQUENCES: 274  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-1834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/009, 953  
 FILING DATE: 21-Jan-1998  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/036,713  
 FILING DATE: 23-JAN-1997  
 APPLICATION NUMBER: US 60/037,432  
 FILING DATE: 07-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weber, Ellen Lauver  
 REGISTRATION NUMBER: 32,762  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-576-0200  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 230:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 230:  
 US-09-009-953-230

Query Match Best Local Similarity 40.7%; Score 37; DB 2; Length 16;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWDPGKQLY 12  
 Db 6 NMWQEVGRAMY 16

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REFERENCE/DOCKET NUMBER: 19729Y  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 908-594-3905  
 TELEFAX: 908-594-4720  
 INFORMATION FOR SEQ ID NO: 40:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
 US-09-340-798A-40

Query Match Best Local Similarity 45.5%; Score 37; DB 2; Length 16;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWDPGKQLY 12  
 Db 5 NMWQEVGRAMY 15

RESULT 10  
 US-09-311-784A-308  
 ; Sequence 308, Application US/09311784A  
 ; Patent No. 653462  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fukes, John D.  
 ; APPLICANT: Hermanson, Gary G.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Ishioka, Glenn Y.  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Chasnoff, Robert W.  
 ; APPLICANT: Epimmune Inc.  
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an  
 ; Immune Response and Methods of Using the Same  
 ; FILE REFERENCE: 39863-20022.01  
 ; CURRENT APPLICATION NUMBER: US/09/311/784A  
 ; CURRENT FILING DATE: 1999-05-13  
 ; PRIOR APPLICATION NUMBER: US 60/085,751  
 ; PRIOR FILING DATE: 1998-05-15  
 ; NUMBER OF SEQ ID NOS: 463  
 ; SOFTWARE: Fast-SEQ for Windows Version 3.0  
 ; SEQ ID NO: 308  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: HIV1 ENV 566 (peptide F091.15)  
 US-09-311-784A-308

Query Match Best Local Similarity 45.5%; Score 37; DB 2; Length 16;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWDPGKQLY 12  
 Db 6 NMWQEVGRAMY 16

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RESULT 11  
 US-09-724-961-51  
 ; Sequence 51, Application US/09724961  
 ; Patent No. 6743427  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schenk, Dale B.  
 ; APPLICANT: Bard, Frederick  
 ; APPLICANT: Vasquez, Nichi  
 ; APPLICANT: Yenock, Ted  
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
 ; FILE REFERENCE: 15270J-004750UC  
 ; CURRENT APPLICATION NUMBER: US/09/724, 961

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/340,798A  
 FILING DATE: 28-Jun-1999  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/877,418  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAND, J. MARK  
 REGISTRATION NUMBER: 36,545

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; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR APPLICATION NUMBER: US 09/322,430
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 51
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:HIV gp120 T1
US-09-724-961-51

Query Match Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 NRWEDPGKOLY 12
Db 5 NMWQEVGKAMY 15
RESULT 14
US-09-862-849-1
; Sequence 1, Application US/09862849
; Patent No. 6855528
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Larry J. Smith
; APPLICANT: Gennady Gololobov
; TITLE OF INVENTION: Methods for Identifying Inducers and Inhibitors of Proteolytic
; APPLICANT: Antibodies, Compositions and Their Uses
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: UNNC 63123 DIV
; CURRENT APPLICATION NUMBER: US/09/862,849
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/046,373
; PRIOR FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus-1
US-09-862-849-1

Query Match Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 NRWEDPGKOLY 12
Db 5 NMWQEVGKAMY 15
RESULT 15
US-10-114-716A-1
; Sequence 1, Application US/10114716A
; Patent No. 6855804
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Yasuhiro Nishiyama
; TITLE OF INVENTION: Covalently Reactive Transition State
; TITLE OF INVENTION: Analogs and Methods of Use Thereof
; FILE REFERENCE: UTH001HB
; CURRENT APPLICATION NUMBER: US/10/114,716A

RESULT 13
US-09-724-551-51
Sequence 51, Application US/09724551
; Patent No. 6787337
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.

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; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/862,849
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/046,373
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/280,624
; PRIOR FILING DATE: 2001-03-31
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ For Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus-1
; US-10-114-716A-1

Query Match      40.7%;  Score 37;  DB 2;  Length 16;
Best Local Similarity 45.5%;  Pred. No. 11;
Matches      5;  Conservative 3;  Mismatches 3;  Indels 0;  Gaps 0;
Qy          2 NRWEDPGKQLY 12
           |::|::|::|
Db          5 NMWQEVGKAMY 15
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Job time : 46 secs

GenCore version 5.1.8  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Om protein - protein search, using sw model.

Run on: May 15, 2006, 16:50:07 ; Search time 159 Seconds

(without alignments)  
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Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNRWEDPGKOLYNVEA 16

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 16

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	91	100.0	16	5 US-10-795-081A-1	Sequence 1, Appli
3	91	100.0	16	6 US-11-066-697-1536	Sequence 1536, Ap
4	37	40.7	16	3 US-09-775-805-44	Sequence 44, Appli
5	37	40.7	16	3 US-09-775-805-67	Sequence 67, Appli
6	37	40.7	16	3 US-09-775-805-75	Sequence 75, Appli
7	37	40.7	16	3 US-09-775-805-89	Sequence 89, Appli
8	37	40.7	16	3 US-09-862-849-1	Sequence 1, Appli
9	37	40.7	16	3 US-09-894-199	Sequence 199, App
10	37	40.7	16	3 US-09-894-594-66	Sequence 66, Appli
11	37	40.7	16	4 US-10-103-395-30	Sequence 230, App
12	37	40.7	16	4 US-10-114-716A-1	Sequence 1, Appli
13	37	40.7	16	4 US-10-041-414-42	Sequence 42, Appli
14	37	40.7	16	4 US-10-372-525-108	Sequence 306, App
15	37	40.7	16	4 US-10-371-069-308	Sequence 308, App
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17	37	40.7	16	4 US-10-371-260-308	Sequence 308, App
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19	37	40.7	16	4 US-10-372-111-9	Sequence 9, Appli
20	37	40.7	16	4 US-10-699-517-11	Sequence 11, Appli
21	37	40.7	16	4 US-10-698-099-11	Sequence 11, Appli
22	37	40.7	16	4 US-10-753-339-44	Sequence 44, Appli
23	37	40.7	16	4 US-10-753-339-67	Sequence 67, Appli
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25	37	40.7	16	4 US-10-753-339-89	Sequence 89, Appli
26	37	40.7	16	4 US-10-771-174A-10	Sequence 10, Appli
27	37	40.7	16	5 US-10-889-999-51	Sequence 51, Appli

#### ALIGNMENTS

RESULT 1  
 US-09-865-281A-1  
 ; Sequence 1, Application US/09865281A  
 ; Publication No. US20030103984A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kohler, Heinz  
 ; TITLE OF INVENTION: FUSION PROTEINS OF BIOLOGICALLY ACTIVE PEPTIDES AND ANTIBODIES  
 ; FILE REFERENCE: 411\_35629PC2  
 ; CURRENT APPLICATION NUMBER: US/09-865-281A  
 ; CURRENT FILING DATE: 2001-05-29  
 ; PRIORITY APPLICATION NUMBER: 09/070,907  
 ; PRIORITY FILING DATE: 1998-05-04  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 1  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)-(16)  
 ; OTHER INFORMATION: synthesized peptide with sequence derived from position 1217-123  
 US-09-865-281A-1  
 Query Match 100.0%; Score 91; DB 3; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKOLYNVEA 16  
 Db 1 KNRWEDPGKOLYNVEA 16

RESULT 2  
 US-10-795-081A-1  
 ; Sequence 1, Application US/10795081A  
 ; Publication No. US2005003303A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kohler, Heinz  
 ; TITLE OF INVENTION: TRANS-MEMBRANE-ANTIBODY INDUCED INHIBITION OF APOPTOSIS  
 ; FILE REFERENCE: 411\_35629AP3  
 ; CURRENT APPLICATION NUMBER: US/10/795,081A  
 ; CURRENT FILING DATE: 2004-01-05  
 ; PRIORITY APPLICATION NUMBER: 60/451,980  
 ; PRIORITY FILING DATE: 2003-03-05  
 ; PRIORITY APPLICATION NUMBER: 09/865,281  
 ; PRIORITY FILING DATE: 2001-05-29  
 ; PRIORITY APPLICATION NUMBER: 09/070,907  
 ; PRIORITY FILING DATE: 1998-05-04  
 ; NUMBER OF SEQ ID NOS: 14

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)::(16)
; OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-1232
US-10-795-081A-1

Query Match 100.0%; Score 91; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKOLYNEVA 16
Db 1 KNRWEDPGKOLYNEVA 16

RESULT 3
US-11-066-697-1536
Sequence 1536, Application US/11066697
Publication No. US2005018759A1
GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Miiner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudieu, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/651,276
; PRIOR FILING DATE: 2000-09-07
; SEQ ID NO 1536
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1536

Query Match 100.0%; Score 91; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKOLYNEVA 16
Db 1 KNRWEDPGKOLYNEVA 16

RESULT 4
US-09-775-805-44
Sequence 44, Application US/09775805
Publication No. US200100361A1
GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-548
; CURRENT APPLICATION NUMBER: US/09/775,805
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1
; OTHER INFORMATION: Th-dominant/subdominant CTL epitopes in MVA.
; OTHER INFORMATION: Th-dominant/subdominant CTL epitopes in MVA.

Query Match 100.0%; Score 37; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy 2 NRWEDPGKQLY 12  
 Db 5 NMWQEVGKAMY 15

**RESULT 7**  
 US-09-775-805-89  
 i Sequence 89, Application US/09775805  
 i GENERAL INFORMATION:  
 i APPLICANT: DUKE UNIVERSITY  
 i TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE  
 i CURRENT APPLICATION NUMBER: US/09/775,805  
 i CURRENT FILING DATE: 2001-02-05  
 i PRIOR APPLICATION NUMBER: 09/497,497  
 i PRIOR FILING DATE: 2000-02-04  
 i NUMBER OF SEQ ID NOS: 107  
 i SOFTWARE: PatentIn Ver. 2.1  
 i SEQ ID NO: 89  
 i LENGTH: 16  
 i TYPE: PRT  
 i ORGANISM: Artificial Sequence  
 i FEATURE:  
 i OTHER INFORMATION: Description of Artificial Sequence: HIV-1 Th-CTL  
 i OTHER INFORMATION: A2 P17 epitope (A2 Variants) in MVA  
 US-09-775-805-89

Query Match Score 37; DB 3; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 76;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12  
 Db 5 NMWQEVGKAMY 15

**RESULT 8**  
 US-09-862-849-1  
 i Sequence 1, Application US/09862849  
 i Patent No. US20020011274A1  
 i GENERAL INFORMATION:  
 i APPLICANT: Sudhir, Paul  
 i APPLICANT: Larry J. Smith  
 i APPLICANT: Gennady Golobov  
 i TITLE OF INVENTION: Methods for Identifying Inducers and Inhibitors of Proteolytic  
 i Title of Invention: Antibodies, Compositions and Their Uses  
 i CURRENT APPLICATION NUMBER: US/09/862,849  
 i CURRENT FILING DATE: 2001-08-29  
 i PRIOR APPLICATION NUMBER: US 09/046,373  
 i PRIOR FILING DATE: 1998-03-23  
 i NUMBER OF SEQ ID NOS: 10  
 i SOFTWARE: FastSEQ for Windows Version 3.0  
 i SEQ ID NO: 1  
 i LENGTH: 16  
 i TYPE: PRT  
 i ORGANISM: Human Immunodeficiency Virus-1  
 US-09-862-849-1

Query Match Score 37; DB 3; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 76;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12  
 Db 5 NMWQEVGKAMY 15

**RESULT 9**  
 US-09-894-018-199  
 i Sequence 199, Application US/09894018

Query Match Score 37; DB 3; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 76;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

---

; Patent No. US20020119127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EPTIMINE, Inc.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Chestnut, Robert  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Baker, Denis  
 ; APPLICANT: Newman, Mark  
 ; APPLICANT: Brown, David  
 ; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
 ; TITLE OF INVENTION: MINIGENS AND PEPTIDES THEREBY  
 ; FILE REFERENCE: 39863-20033.00  
 ; CURRENT APPLICATION NUMBER: US/09/894,018  
 ; CURRENT FILING DATE: 2001-06-27  
 ; PRIOR APPLICATION NUMBER: PCT/US00/35568  
 ; PRIOR FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/173,390  
 ; PRIOR FILING DATE: 1999-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/284,221  
 ; PRIOR FILING DATE: 2001-04-16  
 ; NUMBER OF SEQ ID NOS: 368  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 199  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Transgenic mouse  
 US-09-894-018-199

Query Match Score 40.7%; DB 3; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 76;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12  
 Db 6 NMWQEVGKAMY 16

**RESULT 10**  
 US-09-894-594-66  
 i Sequence 66, Application US/09894594  
 i Publication No. US20030017497A1  
 i GENERAL INFORMATION:  
 i APPLICANT: Kleber-Emmons, Thomas  
 i APPLICANT: Weiner, David B.  
 i APPLICANT: Monzavi-Kazhassi, Behjatolah  
 ; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Encoded by Genes  
 ; TITLE OF INVENTION: Same  
 ; FILE REFERENCE: UPN-3984  
 ; CURRENT APPLICATION NUMBER: US/09/894,594  
 ; CURRENT FILING DATE: 2001-06-28  
 ; PRIOR APPLICATION NUMBER: 09/601,558  
 ; PRIOR FILING DATE: 2000-11-07  
 ; PRIOR APPLICATION NUMBER: PCT/US99/02405  
 ; PRIOR FILING DATE: 1999-02-04  
 ; PRIOR APPLICATION NUMBER: 60/073,690  
 ; PRIOR FILING DATE: 1998-02-04  
 ; PRIOR APPLICATION NUMBER: 60/214,517  
 ; PRIOR FILING DATE: 2000-06-28  
 ; NUMBER OF SEQ ID NOS: 70  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 66  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Novel Sequence  
 US-09-894-594-66

Query Match Score 40.7%; DB 3; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 76;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy            2 NRWEDPGKQLY 12  
           |::| :| :| :|  
           5 NMWQEVGKAMY 15

Db            Qy            2 NRWEDPGKQLY 12  
           |::| :| :| :|  
           5 NMWQEVGKAMY 15

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RESULT 11  
US-10-103-395-230  
; Sequence 230, Application US/10103395  
; Publication No. US20020160019A1  
; GENERAL INFORMATION:  
;   APPLICANT: EPIMMUNE, Inc.  
;   APPLICANT: Sette, Alessandro  
;   APPLICANT: Sidney, John  
;   APPLICANT: Southwood, Scott  
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR  
; FILE REFERENCE: 9963-20016.01  
; CURRENT FILING DATE: 2003-01-03  
; PRIORITY NUMBER: US 09/009, 953  
; PRIORITY APPLICATION NUMBER: PCT/US98/01373  
; PRIORITY FILING DATE: 1998-01-21  
; PRIORITY NUMBER: US 60/036, 713  
; PRIORITY FILING DATE: 1997-01-23  
; PRIORITY APPLICATION NUMBER: US 60/037, 432  
; PRIORITY FILING DATE: 1997-01-07  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 230  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-103-395-230  
Query Match    40.7%;    Score 37;    DB 4;    Length 16;  
Best Local Similarity    45.5%;    Pred. No. 76;  
Matches    5;    Conservative    3;    Mismatches    3;    Indels    0;    Gaps    0;

Qy            2 NRWEDPGKQLY 12  
           |::| :| :| :|  
           6 NMWQEVGKAMY 16

Db            Qy            2 NRWEDPGKQLY 12  
           |::| :| :| :|  
           5 NMWQEVGKAMY 15

---

RESULT 12  
US-10-114-716A-1  
; Sequence 1, Application US/10114716A  
; Publication No. US20030078203A1  
; GENERAL INFORMATION:  
;   APPLICANT: Sudhir, Paul  
;   APPLICANT: Yasubiro Nishiyama  
; TITLE OF INVENTION: Covalently Reactive Transition State  
; FILE REFERENCE: UTH001HB  
; CURRENT FILING DATE: 2002-04-01  
; PRIORITY NUMBER: US/10/114, 716A  
; PRIORITY FILING DATE: 2001-05-22  
; PRIORITY NUMBER: 09/862, 849  
; PRIORITY APPLICATION NUMBER: 09/046, 373  
; PRIORITY FILING DATE: 1998-03-23  
; PRIORITY NUMBER: 60/280, 624  
; PRIORITY FILING DATE: 2001-03-31  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO: 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus-1  
US-10-114-716A-1  
Query Match    40.7%;    Score 37;    DB 4;    Length 16;  
Best Local Similarity    45.5%;    Pred. No. 76;  
Matches    5;    Conservative    3;    Mismatches    3;    Indels    0;    Gaps    0;

; APPLICANT: Chesnut, Robert W.  
 ; APPLICANT: Epimmune Inc.  
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an  
 ; Immune Response and Methods of Using the Same  
 ; FILE REFERENCE: 399c3-20022.01  
 ; CURRENT APPLICATION NUMBER: US/10/371,525  
 ; CURRENT FILING DATE: 2003-02-21  
 ; PRIOR APPLICATION NUMBER: US 09/311,784  
 ; PRIOR FILING DATE: 1999-05-13  
 ; PRIOR APPLICATION NUMBER: US 60/085,751  
 ; PRIOR FILING DATE: 1998-05-15  
 ; NUMBER OF SEQ ID NOS: 463  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 308  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: HIV1 ENV 566 (peptide F091.15)  
 US-10-371-525-308

Query Match 40.7%; Score 37; DB 4; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 76;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 NRWEDPGKLY 12  
 Db 6 NMHQEVGKAMY 16

RESULT 15  
 US-10-371-069-308  
 ; Sequence 308, Application US/10371069  
 ; Publication No. US20030216342A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EPIMMUNE Inc.  
 ; APPLICANT: Fikes, John D.  
 ; APPLICANT: Hermanson, Gary G.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Ishioka, Glenn Y.  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Chesnut, Robert W.  
 ; APPLICANT: Epimmune Inc.  
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an  
 ; Immune Response and Methods of Using the Same  
 ; FILE REFERENCE: 399c3-20022.10  
 ; CURRENT APPLICATION NUMBER: US/10/371,069  
 ; CURRENT FILING DATE: 2003-02-21  
 ; PRIOR APPLICATION NUMBER: US 09/078,904  
 ; PRIOR FILING DATE: 1998-05-13  
 ; PRIOR APPLICATION NUMBER: US 60/085,751  
 ; PRIOR FILING DATE: 1998-05-15  
 ; NUMBER OF SEQ ID NOS: 463  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 308  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: HIV1 ENV 566 (peptide F091.15)  
 US-10-371-069-308

Query Match 40.7%; Score 37; DB 4; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 76;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 NRWEDPGKLY 12  
 Db 6 NMHQEVGKAMY 16

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**Copyright (c) 1993 - 2006 Biocceleration Ltd.**  
**I protein - protein search, using SW model**  
**on: May 15, 2006, 16:51:11 ; Search time 27 Seconds**  
**(without alignments)**  
**27.822 Million cell updates/sec**  
**title: US-09-865-281A-1**  
**perfect score: 91**  
**sequence: 1 KNRWEDPGKOLYNVEA 16**  
**scoring table: BLOSUM62**  
**Gapop 10.0 , Gapext 0.5**  
**searched: 250354 seqs, 46948837 residues**  
**total number of hits satisfying chosen parameters: 2020**  
**minimum DB seq length: 16**  
**maximum DB seq length: 16**

DOCUMENTS

RESULT 1  
US-10-973-977-44  
; Sequence 44, Application US/10973977  
; Publication No. US20060008467A1  
; GENERAL INFORMATION:  
; APPLICANT: HAYNES, BARTON F.  
; APPLICANT: LIAO, HUA-XIN  
; APPLICANT: LETVIN, NORMAN  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE

Published Applications AA\_New:  
\* /SIDSS5\_ptodata/1/pubpa/us08 NEW PUB.pep1:  
\* /SIDSS5\_ptodata/1/pubpa/us06 NEW PUB.pep:  
\* /SIDSS5\_ptodata/1/pubpa/us07 NEW PUB.pep:  
\* /SIDSS5\_ptodata/1/pubpa/us08 NEW PUB.pep:  
\* /SIDSS5\_ptodata/1/pubpa/us09 NEW PUB.pep:  
\* /SIDSS5\_ptodata/1/pubpa/us10 NEW PUB.pep:  
\* /SIDSS5\_ptodata/1/pubpa/us05 NEW PUB.pep:  
\* /SIDSS5\_ptodata/1/pubpa/us09 NEW PUB.pep1:  
\* /SIDSS5\_ptodata/1/pubpa/us10 NEW PUB.pep:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

Result No.	Score	Query Match	Length	DB ID	Description	
					%	SUMMARIES
1	37	40.7	16	9	US-10-973-977-44	Sequence 44, Appl
2	37	40.7	16	9	US-10-973-977-57	Sequence 67, Appl
3	37	40.7	16	9	US-10-973-977-75	Sequence 75, Appl
4	37	40.7	16	9	US-10-973-977-89	Sequence 89, Appl
5	37	40.7	16	11	US-11-045-024-14479	Sequence 14479, Appl
6	37	40.7	16	11	US-11-115-425-88	Sequence 88, Appl
7	37	40.7	16	11	US-11-115-907-11	Sequence 11, Appl
8	32	35.2	16	11	US-11-056-950-226	Sequence 226, Appl
9	32	35.2	16	11	US-11-056-950-230	Sequence 230, Appl
10	32	35.2	16	11	US-11-056-950-234	Sequence 234, Appl
11	32	33.0	16	11	US-11-056-950-241	Sequence 241, Appl
12	30	33.0	16	11	US-11-056-950-54	Sequence 54, Appl
13	28	30.8	16	9	US-10-530-061-1652	Sequence 1652, Appl
14	27	29.7	16	11	US-11-056-950-185	Sequence 185, Appl
15	27	29.7	16	11	US-11-056-950-189	Sequence 189, Appl
16	27	29.7	16	11	US-11-056-950-193	Sequence 193, Appl
17	27	29.7	16	11	US-11-056-950-204	Sequence 204, Appl
18	26	28.6	16	11	US-11-056-950-208	Sequence 208, Appl
19	26	28.6	16	11	US-11-056-950-212	Sequence 212, Appl
20	26	28.6	16	11	US-11-056-950-216	Sequence 216, Appl
21	26	28.6	16	11	US-11-056-950-223	Sequence 223, Appl

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RESULT 1
US-10-973-977-44
; Sequence 44, Application US/10973977
; Publication No. US20060008467A1
; GENERAL INFORMATION
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973, 977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775, 805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497, 497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID. NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-973-977-44

Query Match 40.7% ; Score 37; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4%; Gaps 0;
Matches 5; Conservative 3; Mismatches 3; Indels 0;

On 2 NRWEDPGKOLY 12
;
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RESULT 2  
US-10-973-977-67  
; Sequence 67, Application US/10973977  
; Publication No. US2006008467A1  
; GENERAL INFORMATION:  
; APPLICANT: HAYNES, BARTON F.  
; LIAO, HUA-XIN  
; APPLICANT: LETVIN, NORMAN  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE  
; FILE REFERENCE: 1579-942  
; CURRENT APPLICATION NUMBER: US/10/973-977

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; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 67
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-977-67

Query Match          40.7%;  Score 37;  DB 9;  Length 16;
Best Local Similarity 45.5%;  Pred. No. 6.4;
Matches      5;  Conservative 3;  Mismatches 3;  Indels 0;  Gaps 0;
Qy           2 NRWEDPGKQLY 12
Db           5 NMWQEVGKAMY 15

RESULT 5
US-11-045-024-14479
; Sequence 14479, Application US/11045024
; Publication No. US20050211676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Calis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060_0040007
; CURRENT APPLICATION NUMBER: US/10/973,977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 75
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1
; OTHER INFORMATION: Th-dominant/subdominant CTL epitopes in MVA.
US-10-973-977-75

Query Match          40.7%;  Score 37;  DB 9;  Length 16;
Best Local Similarity 45.5%;  Pred. No. 6.4;
Matches      5;  Conservative 3;  Mismatches 3;  Indels 0;  Gaps 0;
Qy           2 NRWEDPGKQLY 12
Db           5 NMWQEVGKAMY 15

RESULT 5
US-11-045-024-14479
; Sequence 14479, Application US/11045024
; Publication No. US20050211676A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 75
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1
; OTHER INFORMATION: Th-dominant/subdominant CTL epitopes in MVA.
US-10-973-977-75

Query Match          40.7%;  Score 37;  DB 9;  Length 16;
Best Local Similarity 45.5%;  Pred. No. 6.4;
Matches      5;  Conservative 3;  Mismatches 3;  Indels 0;  Gaps 0;
Qy           2 NRWEDPGKQLY 12
Db           5 NMWQEVGKAMY 15

RESULT 4
US-10-973-977-89
; Sequence 89, Application US/10973977
; Publication No. US20060008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 14479
; LENGTH: 16
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY
US-11-045-024-14479

Query Match          40.7%;  Score 37;  DB 11;  Length 16;
Best Local Similarity 45.5%;  Pred. No. 6.4;
Matches      5;  Conservative 3;  Mismatches 3;  Indels 0;  Gaps 0;
Qy           2 NRWEDPGKQLY 12
Db           6 NMWQEVGKAMY 16

```

RESULT 6  
US-11-115-425-88  
Sequence 88, Application US/11115425  
; Publication No. US20060018881A1  
GENERAL INFORMATION:  
APPLICANT: Shiver, John W  
Liu, Margaret A  
PRIORITY: Helen C  
TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. Mark Hand  
STREET: 126 Lincoln Avenue, P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/115,425  
FILING DATE: 27-Apr-2005  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hand, J. Mark  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 19188YCB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (732) 594-1905  
TELEFAX: (732) 594-4720  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 88:  
US-11-115-425-88

Query Match 40.7%; Score 37; DB 11; Length 16;  
Best Local Similarity 45.5%; Pred. No. 64;  
Matches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12  
Db 5 NMWQEYKAMY 15

RESULT 7  
US-11-185-907-11  
Sequence 11, Application US/11185907  
; Publication No. US2006058233A1  
GENERAL INFORMATION:  
APPLICANT: Elan Pharmaceuticals, Inc.  
; Regents of the University of California  
APPLICANT: Schenk, Dale B.  
APPLICANT: Masliah, Eliezer  
APPLICANT: Butini, Manuela  
APPLICANT: Chilcote, Tamie  
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SYNUCLEINOPATHIC DISEASE  
FILE REFERENCE: 015270-00895US  
CURRENT APPLICATION NUMBER: US/11/185,907  
CURRENT FILING DATE: 2005-07-19  
PRIOR APPLICATION NUMBER: US 10/915,214  
PRIOR FILING DATE: 2004-08-09

Query Match 40.7%; Score 37; DB 11; Length 16;  
Best Local Similarity 45.5%; Pred. No. 64;  
Matches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12  
Db 5 NMWQEYKAMY 15

RESULT 8  
US-11-056-950-226  
Sequence 226, Application US/11056950  
; Publication No. US20060035242A1  
GENERAL INFORMATION:  
APPLICANT: MICHLITSCH, Melissa D  
TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS  
FILE REFERENCE: 2300-21026-20  
CURRENT APPLICATION NUMBER: US/11/056,950  
CURRENT FILING DATE: 2005-02-11  
PRIOR APPLICATION NUMBER: 10/917,646  
PRIOR FILING DATE: 2004-08-13  
PRIOR APPLICATION NUMBER: 60/586,509  
PRIOR FILING DATE: 2004-07-09  
PRIOR APPLICATION NUMBER: 60/570,368  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/494,962  
PRIOR FILING DATE: 2003-08-13  
NUMBER OF SEQ ID NOS: 260  
SOFTWARE: Patentin Version 3.3  
SEQ ID NO 226  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: peptide  
US-11-056-950-226

Query Match 40.7%; Score 37; DB 11; Length 16;  
Best Local Similarity 45.5%; Pred. No. 64;  
Matches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKOLYNE 15  
Db 3 NQWNKPSKPKNMK 16

RESULT 9  
US-11-056-950-230  
Sequence 230, Application US/11056950  
; Publication No. US20060035242A1  
GENERAL INFORMATION:  
APPLICANT: MICHLITSCH, Melissa D  
TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS  
FILE REFERENCE: 2300-21026-20  
CURRENT APPLICATION NUMBER: US/11/056,950  
CURRENT FILING DATE: 2005-02-11  
PRIOR APPLICATION NUMBER: 10/917,646  
PRIOR FILING DATE: 2004-08-13  
PRIOR APPLICATION NUMBER: 60/586,509

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; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SEQ ID NO: 230
; SOFTWARE: PatentIn version 3.3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide
US-11-056-950-230

Query Match Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 2 NRWEDPGKQLYNVE 15
Db 2 NQWNKESKPKNMK 15

RESULT 10
US-11-056-950-234
; Sequence 234 Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELIITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 234
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide
US-11-056-950-234

Query Match Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 2 NRWEDPGKQLYNVE 15
Db 2 NQWNKESKPKNMK 15

RESULT 11
US-11-056-950-241
; Sequence 241 Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELIITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 241
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide
US-11-056-950-241

Query Match Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 2 NRWEDPGKQLYNVE 15
Db 2 NQWNKESKPKNMK 15

RESULT 12
US-11-056-950-54
; Sequence 54 Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELIITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 3300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide
US-11-056-950-54

Query Match Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 95;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 2 NRWEDPGKQLYNVE 13
Db 5 NQWNKESKPKNMK 16

RESULT 13
US-10-530-061-1652
; Sequence 1652 Application US/10530061
; Publication No. US20060079453A1
; GENERAL INFORMATION:
; APPLICANT: SIDNEY, JOHN
; APPLICANT: SOUTHWOOD, SCOTT
; APPLICANT: SETTE, ALESSANDRO
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; CURRENT APPLICATION NUMBER: US/10530061
; FILE REFERENCE: 060-1330524E2/MS-M

```

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; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31308
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/416,207
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/417,269
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 2503
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1652.
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-10-530-061-1652

Query Match      30.8%; Score 28; DB 9; Length 16;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy          4 WEDGKQ 10
Db          4 WNHFGSQ 10

RESULT 14
US-11-056-950-185
; Sequence 185, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELI TSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; CURRENT APPLICATION NUMBER: US/11/056,950
; FILE REFERENCE: 2300-21036.20
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 10/917,646
PRIOR FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: 60/586,509
PRIOR FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/570,368
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/494,962
PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
US-11-056-950-185

Query Match      29.7%; Score 27; DB 11; Length 16;
Best Local Similarity 28.6%; Pred. No. 3e+02;
Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy          2 NRWEDPGKQLYNVE 15
Db          2 SQMNKPSPKPKTNMK 15

RESULT 15
US-11-056-950-189
; Sequence 189, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELI TSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; CURRENT APPLICATION NUMBER: US/11/056,950
; FILE REFERENCE: 2300-21036.20
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 10/917,646
PRIOR FILING DATE: 2004-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
US-11-056-950-189

Query Match      29.7%; Score 27; DB 11; Length 16;
Best Local Similarity 28.6%; Pred. No. 3e+02;
Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy          2 NRWEDPGKQLYNVE 15
Db          3 SQMNKPSPKPKTNMK 16

```

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:35:21 ; Search time 38 Seconds  
(without alignments)  
40.512 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNRWDPGKOLYNEA 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : PIR\_80:\*

1: pi1:\*

2: pi2:\*

3: pi3:\*

4: pi4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	30.8	16	G24304	ribosomal protein
2	23	25.3	16	A31963	pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (fragment)
3	22	24.2	16	PT0282	Ig heavy chain CDR
4	20	22.0	16	MTDFBS	melanotropin beta
5	19	20.9	16	D49021	Ig heavy chain J7
6	19	20.9	16	PL0137	protein kinase, 80
7	19	20.9	16	B44896	heat shock protein
8	18	19.8	16	B47014	ori2' 3' of chur -
9	18	19.8	16	PH0773	T-cell receptor be
10	18	19.8	16	A48630	bohorajarac - ja
11	18	19.8	16	S13898	alkaline phosphatase
12	17	18.7	16	B60560	formyltetrahydrofo
13	17	18.7	16	PH0137	T-cell receptor be
14	17	18.7	16	A49255	T-cell receptor be
15	17	18.7	16	B28587	T-cell receptor be
16	17	18.7	16	F53284	Ig H chain V-D-J r
17	17	18.7	16	PH1604	subtilisin (EC 3.4
18	17	18.7	16	PC1299	malticystatin - to
19	17	18.7	16	A59155	30K allergen - rye
20	17	18.7	16	S38292	protein-tyrosine-p
21	16	17.6	16	C45143	T-cell receptor al-
22	16	17.6	16	H41299	T-cell receptor be
23	16	17.6	16	E53284	T-cell receptor be
24	16	17.6	16	D49037	TCR delta chain V-
25	16	17.6	16	S42237	hypothetical prote
26	16	17.6	16	A20190	hypodermin B - ear
27	16	17.6	16	S54271	GATA-2 protein - A
28	16	17.6	16	I79565	hypothetical TCL3/
29	15	16.5	16	A29541	little gastrin - C

## ALIGNMENTS

RESULT 1						
G24304	ribosomal protein H [validated]	-	Haloarcula marismortui	(fragment)		
C;Species:	Haloarcula marismortui					
C;Date:	19-May-1989 #sequence_revision	19-May-1989 #text_change	21-Jul-2000			
C;Accession:	G24304					
R;Shoham, M.; Dijk, J.; Reinhhardt, R.; Wittmann-Liebold, B.						
FEBS Lett. 204: 323-330, 1986						
A;Title: Purification and characterization of ribosomal proteins from the 30 S subunit						
A;Reference number: A24304						
A;Molecule type: protein						
A;Accession: G24304						
A;Residues: 1-16 < SH0>						
A;Cross-references: UNIPARC:UPI000017AEA2						
C;Keywords: protein biosynthesis; ribosome						
Query Match	30.8%	Score 28;	DB 2;	Length 16;		
Best Local Similarity	55.6%	Pred. No. 2.9e+02;				
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;						
Qy	7 PGKQLYNYE 15					
Db	1 PGNKYNYDE 9					

RESULT 2						
A11963	pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (fragment)					
C;Species:	Ascaris suum (pig roundworm)					
C;Date:	29-Jun-1989 #sequence_revision	29-Jun-1989 #text_change	09-Jul-2004			
C;Accession:	A31963					
R;Thissen, J.; Komuniecki, R.						
J. Biol. Chem. 263: 19092-19097, 1988						
A;Title: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaerobic bacterium <i>Leptospirillum ferrooxidans</i>						
A;Reference number: A31963; MUID:89066711; PMID:31398613						
A;Accession: A31963						
A;Status: Preliminary						
A;Molecule type: protein						
A;Residues: 1-16 < TH1>						
A;Cross-references: UNIPROT:P26267; UNIPARC:UPI000017B69C						
C;Keywords: mitochondrion; oxidoreductase; phosphoprotein						
Query Match	25.3%	Score 23;	DB 2;	Length 16;		
Best Local Similarity	57.1%	Pred. No. 1.9e+03;				
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;						
Qy	6 DPGKQLY 12					
Db	9 DPGNSYY 15					

## RESULT 3

PT0282 Ig heavy chain CDR3 region (clone 4-94A) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT0282  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
 A;Reference number: PT0222; MUID:91108337; PMID:1899102  
 A;Accession: PT0282  
 A;Molecule type: DNA  
 A;Residues: 1-16 <YAM>  
 A;Cross-references: UNIPARC:UPI000017C1DA  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match Score 22; DB 2; Length 16;  
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 WEDPGKQ 10  
 Db 8 WFDPNGQ 14

RESULT 4  
 MTDBPS melanotropin beta - spiny dogfish  
 C;Species: Squalus acanthias (spiny dogfish)  
 C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 09-Jul-2004  
 C;Accession: A01471  
 R;Bennett, H.P.J.; Lowry, P.J.; McMullan, C.; Scott, A.P.  
 Biochem. J. 141, 439-444, 1974  
 A;Title: Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-mel  
 A;Reference number: A90277; MUID:75127390; PMID:4375978  
 A;Accession: A01471  
 A;Molecule type: protein  
 A;Residues: 1-16 <BEN>  
 A;Cross-references: UNIPROT:PO1207; UNIPARC:UPI000012F1C2  
 C;Superfamily: corticotropin-lipotropin  
 C;Keywords: hormone

Query Match Score 20; DB 1; Length 16;  
 Best Local Similarity 60.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RWEDP 7  
 Db 11 RWSVP 15

RESULT 5  
 D49021 Ig heavy chain J7 region - African clawed frog  
 C;Species: Xenopus laevis (African Clawed Frog)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C;Accession: D49021  
 R;Haire, R.N.; Ameniya, C.T.; Suzuki, D.; Litman, G.W.  
 J. Exp. Med. 171, 1721-1737, 1990  
 A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation  
 A;Reference number: A47624; MUID:90237760; PMID:2110243  
 A;Accession: D49021  
 A;Molecule type: mRNA  
 A;Residues: 1-16 <HAI>  
 A;Cross-references: UNIPARC:UPI000017692C  
 C;Superfamily: immunoglobulin V region, immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin

Query Match Score 19; DB 2; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 8.4e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RWEDP 6  
 Db 1 RWED 4

RESULT 6  
 PL0137 protein kinase, 80K - pig (fragment)  
 C;Species: Sus scrofa domesticus (domestic pig)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 18-Jun-1993  
 C;Accession: PL0137  
 R;Dechert, U.; Weber, M.; Weber-Schauffelen, M.; Wollny, E.  
 J. Neurochem. 53, 1266-1275, 1989  
 A;Title: Isolation and partial characterization of an 80,000-dalton protein kinase from  
 A;Reference number: PL0137; MUID:89961455; PMID:2769266  
 A;Accession: PL0137  
 A;Molecule type: protein  
 A;Residues: 1-16 <DEC>  
 A;Cross-references: UNIPARC:UPI0000177D3E  
 C;Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match Score 19; DB 2; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 8.4e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 EDPGK 9  
 Db 12 EDLJK 16

RESULT 7  
 B44896 heat shock protein 18 - Streptomyces albus (fragment)  
 C;Species: Streptomyces albus  
 C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C;Accession: B44896  
 R;Guglielmi, G.; Mazodier, P.; Thompson, C.J.; Davies, J.  
 J. Bacteriol. 173, 7374-7381, 1991  
 A;Title: A survey of the heat shock response in four Streptomyces species reveals two g  
 A;Reference number: A44896; MUID:1682303  
 A;Accession: B44896  
 A;Status: Preliminary  
 A;Molecule type: Protein  
 A;Residues: 1-16 <GUG>  
 A;Cross-references: UNIPROT:Q9R663; UNIPARC:UPI000017AD8C  
 A;Note: sequence extracted from NCBI backbone (NCBIP:65107)

Query Match Score 19; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 8.4e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WEDPGKQL 11  
 Db 6 YENIGAQ 13

RESULT 8  
 B47014 orf23, of chur - Bacteroides thetaiotaomicron (fragment)  
 C;Species: Bacteroides thetaiotaomicron  
 C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994  
 C;Accession: B47014  
 R;Cheng, Q.; Hwa, V.; Salyers, A.A.  
 J. Bacteriol. 174, 7185-7193, 1992  
 A;Title: A locus that contributes to colonization of the intestinal tract by Bacteroides  
 A;Reference number: A47014; MUID:93054330; PMID:1429442  
 A;Accession: B47014  
 A;Status: Preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1-16 <CHE>  
 A;Cross-references: UNIPARC:UPI000017AB49  
 A;Note: sequence extracted from NCBI backbone (NCBIN:118015, NCBIP:118017)

Query Match      19.8%;    Score 18;    DB 2;    Length 16;  
 Best Local Similarity      60.0%;    Pred. No. 1.2e+04;  
 Matches      3;    Conservative      1;    Mismatches      0;    Gaps      0;  
 A;Accession: S13898  
 A;Status: Preliminary  
 A;Molecule type: protein  
 A;Residues: 1-16 <FUD>  
 A;Cross-references: UNIPARC:UPI000017C5B6  
 C;Keywords: phosphoric monoester hydrolase

Query Match      19.8%;    Score 18;    DB 2;    Length 16;  
 Best Local Similarity      100.0%;    Pred. No. 1.2e+04;  
 Matches      3;    Conservative      0;    Mismatches      0;    Gaps      0;  
 Qy      5 EDP 7  
 Db      7 EDP 9

RESULT 9

T-cell receptor beta chain (C7) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
 C;Accession: PH0773  
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.  
 A;Reference number: PH0746; PMID:1836010  
 A;Accession: PH0773  
 A;Molecule type: mRNA  
 A;Residues: 1-16 <CAS>  
 A;Cross-references: UNIPARC:UPI0000115FC0; EMBL:X60868; NID:950247; PID:CAA43257.1; PID:  
 A;Experimental source:T lymphocyte  
 C;Keywords: T-cell receptor

Query Match      19.8%;    Score 18;    DB 2;    Length 16;  
 Best Local Similarity      50.0%;    Pred. No. 1.2e+04;  
 Matches      5;    Conservative      1;    Mismatches      0;    Gaps      1;  
 A;Accession: B60560  
 A;Molecule type: protein  
 A;Residues: 1-16 <JOH>  
 A;Cross-references: UNIPROT:Q8TBPB; UNIPARC:UPI000017CB07  
 C;Superfamily: 10-formyltetrahydrofolate dehydrogenase  
 C;Keywords: multifunctional enzyme; NADP; oxidoreductase

Query Match      19.8%;    Score 18;    DB 2;    Length 16;  
 Best Local Similarity      40.0%;    Pred. No. 1.8e+04;  
 Matches      2;    Conservative      3;    Mismatches      0;    Gaps      0;  
 Qy      8 GKQLY 12  
 Db      12 GQEYV 16

RESULT 10

bothrojaracin - jararaca (fragment)  
 N;Alternate names: thrombin inhibitor  
 C;Species: Bothrops jararaca [jararaca]  
 C;Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C;Accession: A48630  
 R;Zingalesi, R.B.; Jandrot-Perrus, M.; Guillain, M.C.; Bon, C.  
 Biochemistry 32, 10794-10802, 1993  
 A;Title: Bothrojaracin, a new thrombin inhibitor isolated from Bothrops jararaca venom:  
 A;Reference number: A48630; PMID:94002075; PMID:8399228  
 A;Accession: A48630  
 A;Status: Preliminary  
 A;Molecule type: Protein  
 A;Residues: 1-16 <ZIN>  
 A;Cross-references: UNIPRON:Q9PPZ4; UNIPARC:UPI00000FD244  
 A;Experimental source:venom  
 A;Note: sequence extracted from NCBI backbone (NCBIPR:138787)

Query Match      19.8%;    Score 18;    DB 2;    Length 16;  
 Best Local Similarity      33.3%;    Pred. No. 1.2e+04;  
 Matches      3;    Conservative      1;    Mismatches      5;    Indels      0;    Gaps      0;  
 A;Accession: B60560  
 A;Molecule type: mRNA  
 A;Residues: 1-16 <MAR>  
 A;Cross-references: UNIPARC:UPI000017C3AF  
 C;Keywords: T-cell receptor

Query Match      19.8%;    Score 18;    DB 2;    Length 16;  
 Best Local Similarity      27.3%;    Pred. No. 1.8e+04;  
 Matches      3;    Conservative      3;    Mismatches      5;    Indels      0;    Gaps      0;  
 Qy      2 NRWEDPKQLY 12  
 Db      6 SRKDSPSPLH 16

RESULT 11

S13898  
 alkaline phosphatase (EC 3.1.3.1) - rabbit  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S13898  
 R;Fujimori-Krai, Y.; Koyama, I.; Hirano, K.; Sakagishi, Y.; Komoda, T.  
 Arch. Biochem. Biophys. 284, 320-325, 1991  
 A;Title: Purification and partial characterization of intestinal-like alkaline phosphatase

RESULT 12

S13898  
 T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997

C;Accession: A49255  
 R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.  
 Eur. J. Immunol. 22, 541-549, 1992  
 A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using  
 A;Reference number: A49039; MUID:92164737; PMID:1311263  
 A;Accession: A49255  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: nucleic acid  
 A;Residues: 1-16 <ROS>  
 A;Cross-references: UNIPARC:UPI000017C3B9  
 A;Note: sequence extracted from NCBI backbone (NCBIP:90722)  
 C;Keywords: T-cell receptor

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Query Match      18.7%; Score 17; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy      7 PGKQ 10
          |||
Db      6 PGTQ 9
```

## RESULT 15

B28587  
 T-cell receptor beta-2 chain J-B2.3 segment - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Accession: B28587  
 C;Sequence\_revision: 16-Aug-1988 #text\_change 05-Nov-1999  
 R;Yononaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
 A;Title: Organization and sequences of the diversity, joining, and constant region genes  
 A;Reference number: A91081; MUID:86094276; PMID:386244  
 A;Accession: B28587  
 A;Molecule type: DNA  
 A;Residues: 1-16 <TOY>  
 A;Cross-references: UNIPARC:UPI000002FD06; GB:M14159; NID:g338852; PIDN:AAA60677.1; PID:  
 C;Keywords: T-cell receptor

```
Query Match      18.7%; Score 17; DB 2; Length 16;
Best Local Similarity 67.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy      7 PGKQL 11
          |||
Db      9 PGTRL 13
```

Search completed: May 15, 2006, 16:39:41  
 Job time : 39 secs

Scoring table:	BLOSUM62				
Gapop:	10.0 , Gapext: 0.5				
Searched:	2166443 seqs., 705528306 residues				
Total number of hits satisfying chosen parameters:	1144				
Minimum DB seq length:	16				
Maximum DB seq length:	16				
Post-processing:	Minimum Match 0% Maximum Match 100%				
	Listing First 45 summaries				
Database :	Uniprot_05_80:: 1: uniprot_sprot::* 2: uniprot_trembl::*				
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	25	27.5	16	2 Q7DLY3_SOLTU	Q7DLY3 solanum tub
2	22	24.2	16	1 FIBA_RABIT	P14461 oryctolagus
3	22	24.2	16	2 Q9TWG0_ACACA	Q9wco acanthamoeb
4	22	24.2	16	2 Q4TSR1_9SFHN	Q4tsrl erythrobaet
5	22	24.2	16	1 Q69121_ANOSA	Q69121 anolis sagr
6	21	23.1	16	2 O21922_9CAUD	O21922 streptococc
7	20	22.0	16	1 MBLB_SQUAC	P01207 equalus aca
8	20	22.0	16	2 Q9UB66_CANPA	Q9ur86 candida par
9	20	22.0	16	2 Q9N732_HUMAN	Q9yj32 homo sapien
10	19.5	21.4	16	2 Q7W2Z7_PSEAE	Q7w2z7 pseudomonas
11	19	20.9	16	2 Q9UCW4_HUMAN	Q9ucw4 homo sapien
12	19	20.9	16	2 Q5CYF3_SCJUA	Q5cf3 schistosoma
13	19	20.9	16	2 Q7SM54_9DELA	Q7sm54 human t-lym
14	18	19.8	16	2 Q53SB3_HUMAN	Q5sbb3 human
15	18	19.8	16	2 Q7M2K8_RABBIT	Q7m2k8 oryctolagus
16	18	19.8	16	2 Q9T206_SOLTU	Q9t206 solanum tub
17	18	19.8	16	2 Q4QVVA_SCOFO	Q4qvva saccharum o
18	18	19.8	16	2 Q5MG28_COETO	Q5mg28 coeligena t
19	18	19.8	16	2 Q9PR24_BOVINA	Q9pr24 bovis rumin
20	17.5	19.2	16	1 AFP2S_MALPA	P81142 malva parvi
21	17	18.7	16	1 SAL3_DNCMY	P82240 oncorhynchus
22	17	18.7	16	1 Q7S047_NEUCR	Q7s047 neurospora
23	17	18.7	16	2 Q8MM83_9NEOP	Q8mm83 helicoverpa
24	17	18.7	16	2 Q8MM84_9NEOP	Q8mm84 helicoverpa
25	17	18.7	16	2 Q8MM85_9NEOP	Q8mm85 helicoverpa
26	17	18.7	16	2 Q8MMN3_9NEOP	Q8mmn3 helicoverpa
27	17	18.7	16	2 Q8MON5_9NEOP	Q8mon5 helicoverpa
28	17	18.7	16	2 Q4XBS1_PLACH	Q4xbs1 plasmid
29	17	18.7	16	2 Q95M79_HORSE	Q95m79 equus cabal
30	17	18.7	16	2 Q9TR88_BOVIN	Q9tr88 bos taurus
31	17	18.7	16	2 Q7M1V9_LYCSES	Q7m1v9 lycorepnsico

OC Oryctolagus.  
NCB\_TaxID=9986;  
RN PROTEIN SEQUENCE.  
RA Blomback B.; Blomback M.; Grondahl N.J.;  
RT "Studies on fibrinopeptides from mammals.";  
RL Acta Chem Scand. 19:1769-1771(1965).  
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.  
CC -!- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3 nonidentical chains (alpha, beta and gamma). The 2 heterotrimers are in head to head conformation with the N-termini in a small central domain (By similarity).  
CC -!- DOMAIN: A long coiled coil structure formed by 3 polypeptide chains connects the central nodule to the C-terminal domains (distal modules). The long C-terminal ends of the alpha chains fold back, contributing a fourth strand to the coiled coil  
CC -!- PEPTIDE: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC -----  
CC Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.  
KW PEPTIDE 1  
FT 16  
FT 16  
SEQUENCE 16 AA; 1651 MW;  
SQ DFB623279BA55BB6 CRC64;

Query Match Score 22; DB 1; Length 16;  
Best Local Similarity 42.9%; Pred. No. 1.5e+04;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 4  
Q4TSR1\_9SPHN PRELIMINARY;  
ID Q4TSR1\_9SPHN  
AC Q4TSR1;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=EL10115;  
OS Erythrobacter litoralis HTCC2594.  
OC Bacteria; Proteobacteria; Alpha proteobacteria; Spingomonadales; Spingomonadaceae; Erythrobacter.  
NCI\_TaxID=114223;  
OX RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HTCC2594;  
RA Giovannini S.J., Cho J.-C., Ferriera S., Johnson J., Kravitz S., Friedman R., Remington K., Beeson K., Tran B., Rogers Y.-H., Venter J.C.; Friedman R., Venter J.C.;  
RA RFL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.  
DR EMBL: AAGGG01000001; EAL76309.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 16 AA; 1864 MN; 4D15FSFP0BA08A1E CRC64;  
Query Match Score 22; DB 2; Length 16;  
Best Local Similarity 75.0%; Pred. No. 1.5e+04;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RWD 6  
Db 2 RWD 5

RESULT 5  
Q691Z1\_ANOSA  
ID Q691Z1\_ANOSA PRELIMINARY;  
AC Q691Z1;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
OS Anolis sagrei (Brown anole).  
OC Bivalvula; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi; Lepidosaauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.  
OX NCBI\_TaxID=8937;  
RN NUCLOTIDE SEQUENCE.  
RX PubMed:1535629; DOI=10.1018/nature02807;  
RA Kolbe J.J., Gior R.E., Rodriguez Schettino L., Chamizo Lara A., Larson A., Losos J.B.;  
RA "Genetic variation increases during biological invasion by a Cuban lizard.";  
RT Nature 431:177-181(2004).  
RL EMBL: AY655188; AAC78035.1; -; Genomic\_DNA.  
DR GO:GO:0016020; C:membrane; IEA.  
DR GO:GO:0005739; C:mitochondrion; IEA.  
DR GO:GO:0004129; F:cytochrome-c oxidase activity; IEA.  
DR InterPro:IPR000883; COX1.  
DR PANTHER:PTHR10422; COX1; 1.  
KW Mitochondrion.  
FT NON\_TER 16 AA; 1933 MW; B0C8C72FF7483A35 CRC64;  
SQ SEQUENCE 16 AA; 1933 MW;

Query Match Score 22; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 WED 6  
Db 2 WED 4

Qy	2 NRW 4       	2 NRW 4       	Best Local Similarity 60.0%; Pred. No. 3.3e-04; Mismatches 0; Indels 0; Gaps 0;
Db	4 NRW 6		
<hr/>			
RESULT 6			
ID O21922_9CAUD PRELIMINARY;	PRT; 16 AA.		
AC O21922_9CAUD PRELIMINARY;	PRT; 16 AA.		
DT 01-JAN-1998 (TREMBLrel. 05, Created)			
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)			
DB Integrase (Fragment).			
GN Name=nt;			
OS Streptococcus thermophilus bacteriophage Sfi21.			
OC Virus; ssDNA viruses, no RNA stage; Caudovirales; Siphoviridae.			
OX NCBI_TaxID:641867			
RN [1]			
RP NUCLEOTIDE SEQUENCE.			
RX MEDLINE=98008989; PubMed=9344917; DOI=10.1006/viro.1997.8769;			
RA Bruttin A.; Foley S.; Brussow H.;			
RT "The site-specific integration system of the temperate Streptococcus thermophilus bacteriophage phisfi21."			
RT Virology 237:148-158(1997).			
RL Virology 237:148-158(1997).			
DR EMBL; AF013584; AAC48909.1; -; Genomic_DNA.			
DR EMBL; AF013587; AAC48910.1; -; Genomic_DNA.			
FT NON_TER 1 1			
SQ SEQUENCE 16 AA; 1856 MW; 8FA82D3270B9A959 CRC64;			
Query Match Best Local Similarity 23.1%; Score 21; DB 2; Length 16; Matches 3; Conservative 3.3%; Pred. No. 2.2e+04; Indels 0; Gaps 0;			
Qy 1 KNRWEDPGK 9     :   : 1 KQMWTTEGCR 9			
Db			
<hr/>			
RESULT 7			
ID MLB_SQUAC STANDARD; PRT; 16 AA.			
AC P01207_			
DT 01-OCT-2000 (Rel. 01, Created)			
DT 21-JUL-1986 (Rel. 01, Last sequence update)			
DT 05-JUL-2004 (Rel. 44, Last annotation update)			
DB Melanotropin beta.			
OS Squatulus acanthias. (Spiny dogfish).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Clasmodibranchii; Squalea; Hypnosqualea; Squaliformes; Squaloidei; Squatidae; Squatilus.			
OC OC NCBI_TaxID=7797;			
RN [1]			
RP PROTEIN SEQUENCE.			
RX MEDLINE=75127390; PubMed=4375979;			
RA Bennett H.P.J.; Lowry P.J.; McMurtain C.; Scott A.P.;			
RT "Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-melanocyte-stimulating hormone from the neurointermediate lobe of the pituitary of the dogfish Squatulus acanthias.";			
RT Biochem. J. 141:439-44 (1974).			
RL CC - SIMILARITY: Belongs to the POMC family.			
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC DR PIR: A01471; MTDBBS.			
KW Direct protein sequencing; Hormone.			
SQ SEQUENCE 16 AA; 1939 MW; 993AF43C8A640AOE CRC64;			
Query Match Best Local Similarity 22.0%; Score 20; DB 1; Length 16;			
Qy 1 KNRWEDPGKQ 10 :     : 7 RGRKEEGKGE 16			
Db			

RESULT 10	Q7WZ27_PSEAE PRELIMINARY;	PRT;	16 AA.	
ID Q7WZ27;				
AC AC	25, Created	PRT;	16 AA.	
DT 01-OCT-2003	(TREMBLrel. 25, Last sequence update)			
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE Putative radical activating enzyme (Fragment).				
Name=PA0975;				
OS Pseudomonas aeruginosa.				
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;				
OC Pseudomonadaceae; Pseudomonas.				
OX NCBI_TaxID=287;				
RN NUCLEOTIDE SEQUENCE.				
RC STRAIN=PA14; PubMed=14981043; DOI=10.1073/pnas.03104622101;				
RX He J., Baldini R.L., Deziel E., Saucier M., Zhang Q., Liberati N.T., Lee D., Urbach J., Goodman H.M., Rahme L.G.;				
RA "The broad host range pathogen Pseudomonas aeruginosa strain PA14 carries two pathogenicity islands harboring plant and animal virulence genes";				
RT Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535 (2004).				
RL EMBL; AY273870; AAP82945_1; -; Genomic_C-DNA.				
DR AY273870;				
FT NON_TER				
SQ SEQUENCE 16 AA; 1941 MW; 1DDD9BS022AF6B7C CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AY808532; AAX24421_1; -; mRNA.				
FT Hypothetical protein.				
SQ SEQUENCE 16 AA; 1945 MW; 736949EAB699AC65 CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Han Z.; Schistosoma japonicum (Blood fluke); Trematoda; Digenea; Strigeidae; Schistosomatidae; Schistosoma; Metazoa; Platyhelminthes; Trematoda; Digenea; Schistosoma.				
OC Schistosomatidae; Schistosomatidae; Schistosoma.				
NCBI_TaxID=6182;				
RN NUCLEOTIDE SEQUENCE.				
RA Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AY808532; AAX24421_1; -; mRNA.				
FT Hypothetical protein.				
SQ SEQUENCE 16 AA; 1945 MW; 736949EAB699AC65 CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AY808532; AAX24421_1; -; mRNA.				
FT Hypothetical protein.				
SQ SEQUENCE 16 AA; 1945 MW; 736949EAB699AC65 CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AY808532; AAX24421_1; -; Genomic_DNA.				
FT NON_TER				
SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFEE4146EA2F CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Gonzalez Perez M.P., Garcia Saiz A.; Belter E., Korzlowicz A., Dixon R.; Name-SLC4A10; Homo sapiens (Human).				
DR EMBL; AY529962; AAB87693_1; -; Genomic_DNA.				
FT NON_TER				
SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFEE4146EA2F CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AY808532; AAX24421_1; -; Genomic_DNA.				
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SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFEE4146EA2F CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AY808532; AAX24421_1; -; Genomic_DNA.				
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DR EMBL; AY808532; AAX24421_1; -; Genomic_DNA.				
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DR EMBL; AY808532; AAX24421_1; -; Genomic_DNA.				
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RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
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FT NON_TER				
SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFEE4146EA2F CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AY808532; AAX24421_1; -; Genomic_DNA.				
FT NON_TER				
SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFEE4146EA2F CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AY808532; AAX24421_1; -; Genomic_DNA.				
FT NON_TER				
SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFEE4146EA2F CRC64;				
RN NUCLEOTIDE SEQUENCE.				
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
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DR EMBL; AY808532; AAX				

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 RA Watson R.H.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.  
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 RA Watson R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Wilson R.K.;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.  
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 RT "Purification and partial characterization of intestinal-like alkaline  
 phosphatase in rabbit kidney."  
 RL Arch. Biochem. Biophys. 284:320-325 (1991).  
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